

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:26:09 ; Search time 15.01 Seconds
(without alignments)
1096.183 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCGSHVHTKEVKEVA.....LRVNTFNWNTKQEHFPD 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	A45803	B-cell-restricted
2	1085	94.4	289	G00031	B7 protein - red-c
3	738	64.2	299	I46690	CD80 precursor - r
4	601.5	52.3	321	I34766	B-lymphocyte activ
5	561	48.8	309	I49503	B-lymphocyte activ
6	182	15.8	329	A48754	B7-2 antigen - hum
7	152	13.2	309	I49522	gene B7-2 protein
8	140.5	12.2	330	I46691	CD86 precursor - r
9	133.5	11.6	583	I39428	alcam - human
10	129	11.2	221	Q0BE48	BARF1 protein - hu
11	127	11.1	526	I70587	butyrophilin precu
12	122.5	10.7	588	JH0506	adhesion molecule
13	122.5	10.7	588	A45254	surface glycoprote
14	120.5	10.5	509	JC5288	SHP substrate-1 pr
15	120.5	10.5	513	JC5289	SHP substrate-1 pr
16	118	10.3	487	S51333	butyrophilin - mou
17	116.5	10.1	1088	I1XKLN	neural cell adhesi
18	115	10.0	761	IJHUNG	neural cell adhesi
19	112.5	9.8	725	JEO099	neural cell adhesi
20	110.5	9.6	587	JH0464	CD-GRASP precursor
21	109.5	9.5	646	I38049	cell surface glyco
22	109.5	9.5	853	IJBONC	neural cell adhesi
23	109	9.5	526	A37821	butyrophilin - bov
24	109	9.5	2029	1TDFLK	protein-tyrosine-p
25	108	9.4	871	I48696	protein-tyrosine k
26	108	9.4	881	I48697	protein-tyrosine k
27	107.5	9.4	5175	T20992	hypothetical prote
28	107.5	9.4	5198	T43290	hemipterin precurs
29	106.5	9.3	333	A31923	amalgam protein pr

neural cell adhesi
T-cell receptor be
neural cell adhesi
Ig kappa chain V r
T-cell receptor be
neural cell adhesi
neural cell adhesi
fibroblast growth
neural cell adhesi
hypothetical prote
sax-3 protein - Ca
SHP substrate-1 pr
neogenin - chicken
cell adhesion prot
T-cell receptor be

30 106.5 9.3 858 1 IJRTNC
31 106 9.2 267 2 PL0064
32 105.5 9.2 1091 1 IJCHNL
33 104.5 9.1 210 2 A56169
34 104 9.1 307 1 RWM5BC
35 104 9.1 725 2 JEO100
36 104 9.1 1092 1 JN0635
37 103.5 9.0 480 2 A56182
38 103.5 9.0 725 1 IJMSNG
39 103.5 9.0 1115 1 IJMSNL
40 103 9.0 423 2 T29349
41 103 9.0 1273 2 T42405
42 102.5 8.9 503 2 JC5287
43 102 8.9 1443 2 I50600
44 101 8.8 1033 2 S19247
45 100 8.7 309 2 S18894

ALIGNMENTS

RESULT 1
A45803
B-cell-restricted antigen B7 precursor - human
N:Alternate names: B-lymphocyte activation antigen B7
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
C:Accession: I54495; A45803
R:Seivakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
Immunogenetics 36, 175-181, 1992
A:Title: Genomic organization and chromosomal location of the human gene encoding the
A:Reference number: I54495; MUID:92307753
A:Accession: I54495
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-288 <RES>
A:Cross-references: GB:M3077; NID:g179327; PIDN:AAA58390.1; PID:g179329
R:Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.
J. Immunol. 143, 2714-2722, 1989
A:Title: B7, a new member of the Ig superfamily with unique expression on activated a
A:Reference number: A45803; MUID:90010147
A:Accession: A45803
A:Molecule type: mRNA
A:Residues: 1-288 <FRE>
A:Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916
C:Genetics:
A:Gene: GDB:CD80; CD28LGL1; CD28
A:Cross-references: GDB:251792; OMIM:112203
A:Map position: 3q13.3-3q21
A:Introns: 34/1; 140/1; 234/1; 266/1
C:Superfamily: B-lymphocyte restricted antigen B7
C:Keywords: transmembrane protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.5e-86;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGSHVHTKEVKEVATLSCGHVSVVEELAQTQRIYWKQKKVLTWMSGDMNIWPE 60
Db 27 GUSHFCGSHVHTKEVKEVATLSCGHVSVVEELAQTQRIYWKQKKVLTWMSGDMNIWPE 86
QY 61 YKNRTFTDITNLSIVILALRPSDEGTYECVILKYEKDAFKREHLAEVTLVSKADFPPTS 120
Db 87 YKNRTFTDITNLSIVILALRPSDEGTYECVILKYEKDAFKREHLAEVTLVSKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGFFPEPHLSWLENGEELNAINITVTSQDPETELVAVSSKLD 180
Db 147 ISDFEPTSNIRRIICSTSGGFFPEPHLSWLENGEELNAINITVTSQDPETELVAVSSKLD 206
QY 181 NMTTNHSFMCILIKYGLRVNQTFNWNNTKQEHFPD 216

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Db 207 NMTHSFMCCLIKYGLHRLVQNTFNWNTTKQEHFPDN 242
|||||
RESULT 2
G00031
B7 protein - red-crowned mangabey (fragment)
C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031
R:Villinger, F.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: G00217
A:Accession: G00031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <VIL>
A:Cross-references: EMBL:U19833; NID:g644783; PIDN:AAA86700.1; PID:g644784
A:Gene: B7
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 94.4%; Score 1085; DB 2; Length 289;
Best Local Similarity 95.3%; Pred. No. 1.4e-80;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVHVTKEVATLSGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPEY 61
|||||
Db 28 LSHFCSGVHVTKEVATLSGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPEY 87
|||||
QY 62 KNTIFDITNNLSIVILALRPSDEGTGECVWLKYKDAFKREHLAEVTLVSKADFTPSI 121
|||||
Db 88 KNTIFDITNNLSIVILALRPSDEGTGECVWLKYKDAFKREHLAEVTLVSKADFTPSI 147
|||||
QY 122 SFEPTSNIRRICTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLDNF 181
|||||
Db 148 TDFEIPPSNIRRICTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLDNF 207
|||||
QY 182 MTNHSFMCCLIKYGLHRLVQNTFNWNTTKQEHFPDN 216
|||||
Db 208 MTNHSFVCLIKYGLHRLVQNTFNWNTPKQEHFPDN 242
|||||

RESULT 3
I46690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: I46690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: I46689; MUID:95369849
A:Accession: I46690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:g755096; PIDN:BAA08643.1; PID:g755097
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 64.2%; Score 738; DB 2; Length 299;
Best Local Similarity 63.9%; Pred. No. 1.8e-52;
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

QY 4 HFCSGVHVTKEVATLSGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPEYKN 63
|||||
Db 29 H*SSGISQVTSKSVKEMAALSCDYNISIDELARMRIYQKQDQVLSIISGVGVWPEYKN 88
|||||
QY 64 RTIFDITNNLSIVILALRPSDEGTGECVWLKYKDAFKREHLAEVTLVSKADFTPSISD 123
|||||
Db 89 RTFPDITNNLSMLIALRLSDKGYTCVQKNGNSFRRHLTSVTLIRADFVPVSTD 148
|||||

QY 124 FEPTSNIRRICTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLDNFMT 183
|||||
Db 149 IGHPDPNVKIRCSAGSGFPEPLAWMEDGELNAVNTTVDDLDLTLYSVSSSELDNFMT 208
|||||
QY 184 TNHSFMCCLIKYGLHRLVQNTFNWNTTKQEH 211
|||||
Db 209 NNHSIVCLIKYGLSVQSPFWSKPKQEH 236
|||||

RESULT 4
I54766
B-lymphocyte activation antigen 7-1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C:Accession: I54766
R:Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.
Int. Immunol. 7, 171-178, 1995
A:Title: Cloning the rat homolog of the CD28/CTLA-4 ligand B7-1: structural and funct
A:Reference number: I54766; MUID:95252184
A:Accession: I54766
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-321 <RES>
A:Cross-references: EMBL:U05593; NID:g453381; PIDN:AAA80154.1; PID:g453382
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 52.3%; Score 601.5; DB 2; Length 321;
Best Local Similarity 54.4%; Pred. No. 2.2e-41;
Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

QY 1 GLSHFCSGVI-HVTKEVKEVATLSGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIW 59
|||||
Db 31 GLQIISGGIVGVSKSVREKALLSCDYKFCSEERQSIRIYQKDKWLSVSGVPEVWP 90
|||||
QY 60 EYKNTIFDITNNLSIVILALRPSDEGTGECVWLKYKDAFKREHLAEVTLVSKADFTPT 119
|||||
Db 91 KYKNTIVDIANNYSFSLGLILSDRGTYTCVQVREGGSYVVKHLLTVELSVRADFPPT 150
|||||
QY 120 STSDFEPTSNIRRICTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLD 179
|||||
Db 151 NITEYGNPSADIKRITCFASGGFPKPLSWLENGELNINTTISQDPESELYTISSQLD 210
|||||
QY 180 FNMTTNSFMCCLIKYGLHRLVQNTFNW 205
|||||
Db 211 FNATYDHFIDCFIEYGDHVSQNTFW 236
|||||

RESULT 5
I49503
B-lymphocyte activation antigen 7 precursor - mouse
N:Alternate names: MB7-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: I49503; S17291; I49521
R:Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: I49503; MUID:93307789
A:Accession: I49503
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L12589; NID:g293299; PIDN:AAA37240.1; PID:g293301
R:Freeman, G.J.; Gray, G.S.; Gimmi, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Finge
J. Exp. Med. 174, 625-631, 1991
A:Title: Structure, expression, and T cell costimulatory activity of the murine homol
A:Reference number: S17291; MUID:91341422
A:Accession: S17291
A:Molecule type: mRNA
A:Residues: 1-274, 'R', 279-309 <FRES>
A:Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112

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R;Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Uede, T.

Biochem. Biophys. Res. Commun. 200, 443-449, 1994

A:Title: Identification of an alternatively spliced form of the murine homologue of B7.

A:Reference number: I49521; MUID:94220123

A:Accession: I49521

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-143,238-274, R', 279-309 <RE2>

A:Cross-references: GB:D16220; NID:95051118; PIDN:BAA03748.1; PID:g994769

C:Genetics:

A:Gene: B7

A:Introns: 37/1; 143/1; 237/1; 275/1

C:Superfamily: B-lymphocyte restricted antigen B7

C:Keywords: alternative splicing

Query Match 48.8%; Score 561; DB 2; Length 309;
Best Local Similarity 50.7%; Pred. No. 3.9e-38;
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

Qy 12 VTKEVKEVATLSCHNVSVEELAQTRIVWQKEKKVLTMMSGDMNIWPEYKNRTIFDI 71

Db 42 LSKYKRVLLPCRYNSPHEDESDRIYVQKHDKVLSVIAGKLVKWPPEYKNRTLYDNT- 100

Qy 72 NLSIVILALRPSDEGTVCVVKYKDAFKREHLAEVTLVKADPPTPSISDFEIPTSNI 131

Db 101 TYSLLILGLVSDRGTYSCVQKRGTYEVKHLAKLSKADSTNIESGNPSADT 160

Qy 132 RRIICSTSGGPPPEHLSWLENGEELNAINITVSDPETELYSKSLDFNTNHSFACL 191

Db 161 KRITCFASGGPPKPRFSLWNGRELPGINTTISQPESELTYTSSQLDFNTNRHTIKCL 220

Qy 192 IKYGLRVNQTFFNWTQEHFPDN 216

Db 221 IKYGDARVSEDTFWEKPPEDP-PDS 244

RESULT 6

A48754

B7-2 antigen - human

N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A48754; S39055

R:Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard, Science 262, 909-911, 1993

A:Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation

A:Reference number: A48754; MUID:94053735

A:Accession: A48754

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-329 <PRE>

A:Cross-references: GB:L25259; NID:9416368; PIDN:AAA58389.1; PID:g416369

A:Note: It is uncertain whether Met-1 or Met-7 is the initiator

R:Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, C. Nature 366, 76-79, 1993

A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.

A:Reference number: S39055; MUID:94050123

A:Accession: S39055

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 7-329 <AZU>

A:Cross-references: GB:U04343; NID:g439838; PIDN:AAB03814.1; PID:g439839

C:Genetics:

A:Gene: GDB:CD86; CD28LG2

A:Cross-references: GDB:433597; OMIM:601020

A:Map position: 3q13.3-3q21

C:Superfamily: B7-2 antigen

C:Keywords: glycoprotein

Query Match 15.8%; Score 182; DB 1; Length 329;

Best Local Similarity 29.0%; Pred. No. 2e-07;

Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;

Qy 18 EVATLSC---CHNVSVEELAQTRIVWQKEKKVLTMM-----SGDMNIWPEYKNRTIFDI 69

Db 34 ETADLPQOFANSQNSJSELY---VFWDQENLVNLYLGLKEKFDVSVHSYMGRTSFD- 89

Qy 70 TNNLSIVILALRPSDEGTVCVVKYKDAFKREHLAEVTLVKADPPTPSISDFEIPTS 129

Db 90 SDSWTLRHLNLOIKDKGLYQCLIIHHKPTGMIRIHQMSLSVLANSFQPEI---VPIS 145

Qy 130 NIR-----RIICSTSGGPPPEHLSWLENGEELNAINITV-----SQDPETELYS 175

Db 146 NITENVYINLTCSHIGHYPEPKMSVL-----LRTKNSTIEYDGMQKSDQNVTELYDVS 200

Qy 176 SKLDF---NMTNHSFMCILIKYGLRV 199

Db 201 ISLSVSFPDVTNMTIFCILETDKTRL 227

RESULT 7

I49522

gene B7-2 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I49522

R:Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim J. Exp. Med. 178, 2185-2192, 1993

A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell

A:Reference number: I49522; MUID:94065585

A:Accession: I49522

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-309 <RES>

A:Cross-references: GB:L25606; NID:g432478; PIDN:AAA79770.1; PID:g432479

C:Genetics:

A:Gene: B7-2

C:Superfamily: B7-2 antigen

Query Match

Best Local Similarity 13.2%; Score 152; DB 2; Length 309;

Matches 52; Conservative 43; Mismatches 78; Indels 26; Gaps 10;

Qy 20 ATLSC---CHNVSVEELAQTRIVWQKEKKVLTMM-----TMMSGDMNIWPEYKNRTIFDI 69

Db 36 AYLPCTFTRAKNISLSELY---VFWDQQLVLYEHLVGLTEKLDVSN--AKYLGRTSFD- 89

Qy 70 TNNLSIVILALRPSDEGTVCVVKYKDAFKREHLAEVTLVKADPPTPSISDFEIP 127

Db 90 RNNWTLRLHNVTIKMGSDYDCFIQKPPPTGSIILQOTLTE--LSVIANFSEPEIKLAQNV 147

Qy 128 TSNIR--RIICSTSGGPPPEHLSW--LENGEELNAINITVSDPETELYSKSLDFNM-- 182

Db 148 TNSGNIINLTCTSKQHPKPKMYFLITNSTNEYGDNMQISQDNVTFLFSISNLSLSPD 207

Qy 183 -TTNHSFMCILIKYGLRVN 200

Db 208 GYWHMTVVCVLETESMKIS 226

RESULT 8

I46691

CD86 precursor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999

C:Accession: I46691

R:isono, T.; Seto, A. Immunogenetics 42, 217-220, 1995

A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole

A:Reference number: I46689; MUID:95369849

A:Accession: I46691

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Reference number: JH0506; MUID:92030150

A:Accession: JH0506

A:Molecule type: mRNA

A:Residues: 1-588 <TAN>

A:Cross-references: GB:S63276; NID:g238000; PIDN:AAB20170.1; PID:g238001

A:Experimental source: embryo

A:Accession: PS0270

A:Molecule type: protein

A:Residues: 34-48 <TAN1>

C:Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons

C:Keywords: glycoprotein; transmembrane protein

F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-588/Product: adhesion molecule SCL #status predicted <ADH>

F:500-523/Domain: transmembrane #status predicted <TRA>

F:101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 10.7%; Score 122.5; DB 2; Length 588;

Best Local Similarity 25.7%; Pred. No. 0.027;

Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

QY 59 PEYKNTFTDITNNLSIVILALRPDSDEGYECVVLKYEKDAFKREHLAEVTLVSKADPEPT 118

DB 90 PDYKDR--LSLSENYTLISKARISDEKRFVCMVLT-EDDVSEETPVVKV-----FKQ 139

QY 119 PS-----ISDFEIPTSNIRRI-ICSTGGPPEPHLSWLENG-----EELNAINTTVSQ 165

DB 140 PSQPELHQADF-LETEKLMKMGECVVRDSYPEGNTWYKNGRVLPQVVEVVVNLKRVK 198

QY 166 DPETELAVSSKLDNMT---TNHSFMCILIKY 194

DB 199 NRSTGLFTMTSSLOQMPYTKEDANAKFTCIYV 230

RESULT 13

A45254

Surface glycoprotein BEN precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000

C:Accession: A45254; S19202

R:Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992

A:Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in

A:Reference number: A45254; MUID:92302224

A:Accession: A45254

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-588 <POU>

A:Cross-references: EMBL:X64301; NID:g63087; PIDN:CAA45579.1; PID:g63088

C:Keywords: glycoprotein

Query Match 10.7%; Score 122.5; DB 2; Length 588;

Best Local Similarity 25.7%; Pred. No. 0.027;

Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

QY 59 PEYKNTFTDITNNLSIVILALRPDSDEGYECVVLKYEKDAFKREHLAEVTLVSKADPEPT 118

DB 90 PDYKDR--LSLSENYTLISKARISDEKRFVCMVLT-EDDVSEETPVVKV-----FKQ 139

QY 119 PS-----ISDFEIPTSNIRRI-ICSTGGPPEPHLSWLENG-----EELNAINTTVSQ 165

DB 140 PSQPELHQADF-LETEKLMKMGECVVRDSYPEGNTWYKNGRVLPQVVEVVVNLKRVK 198

QY 166 DPETELAVSSKLDNMT---TNHSFMCILIKY 194

DB 199 NRSTGLFTMTSSLOQMPYTKEDANAKFTCIYV 230

RESULT 14

JC5288

SHP substrate-1 protein, 509 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000

C:Accession: JC5288

R:Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka,

Biochem. Biophys. Res. Commun. 231, 61-67, 1997

A:Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localizat

A:Reference number: JC5287; MUID:97223399

A:Contents: Brain

A:Accession: JC5288

A:Molecule type: mRNA

A:Residues: 1-509 <YAM>

A:Cross-references: DDBJ:D87967; NID:g1864012; PIDN:BAA13520.1; PID:g1864013

C:Comment: This protein is a glycosylated receptor-like protein and plays a role in c

acts as a docking protein and induce translocation of SHP-2 from the cytosol to the

C:Genetics:

A:Gene: shps-1

A:Map position: 2

Query Match 10.5%; Score 120.5; DB 2; Length 509;

Best Local Similarity 25.9%; Pred. No. 0.032;

Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

QY 3 SHFCSGV----IHVTKEVKEVA-----TLSCGHNVSVEELAQTRIYKQK---EKKMVL 48

DB 23 SCFCGTGVTGKELKVTQPEKSVSVAAGDSTVLCN---TLTSLLPVGPVKWYRGVQSRLLI 79

QY 49 TMMSGDMNIWPEYKNTFTDIT--NNL--SIVILALRPDSDEGYECVVLKYEKDAFKREH 104

DB 80 YSFTGEH--FPRVTN--VSDATKRNNDFSIRISNTVPEDAGTYTCV--KFQKGPSEPT 133

QY 105 L-----AEVTLVSKADFTPS-ISDFEIPTSNIRRIICSTGGPPEP-HLSWLENGEEL 156

DB 134 ETQSGGTEVYVLAKPSPPEVSGPADRGIPDQKV-NFTCKSHGFSRNTITLWFKDQOEL 192

QY 157 NAINTTVSQDPETELYAVSS--KLPDNMTNHSFMCILIKYHLRVNQT 202

DB 193 HHLETTVPNSGKNVSYNISSTVRVVLNSMDVHS-KVICEVAHTILDRS 239

RESULT 15

JC5289

SHP substrate-1 protein, 513 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000

C:Accession: JC5289

R:Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka,

Biochem. Biophys. Res. Commun. 231, 61-67, 1997

A:Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localizat

A:Reference number: JC5287; MUID:97223399

A:Contents: Bzrain

A:Accession: JC5289

A:Molecule type: mRNA

A:Residues: 1-513 <YAM>

A:Cross-references: DDBJ:D87968; NID:g1864014; PIDN:BAA13521.1; PID:g1864015

C:Comment: This protein is a glycosylated receptor-like protein and plays a role in c

acts as a docking protein and induce translocation of SHP-2 from the cytosol to the

C:Genetics:

A:Gene: shps-1

A:Map position: 2

Query Match 10.5%; Score 120.5; DB 2; Length 513;

Best Local Similarity 25.9%; Pred. No. 0.032;

Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

QY 3 SHFCSGV----IHVTKEVKEVA-----TLSCGHNVSVEELAQTRIYKQK---EKKMVL 48

DB 23 SCFCGTGVTGKELKVTQPEKSVSVAAGDSTVLCN---TLTSLLPVGPVKWYRGVQSRLLI 79

QY 49 TMMSGDMNIWPEYKNTFTDIT--NNL--SIVILALRPDSDEGYECVVLKYEKDAFKREH 104

DB 80 YSFTGEH--FPRVTN--VSDATKRNNDFSIRISNTVPEDAGTYTCV--KFQKGPSEPT 133

Search completed: April 24, 2002, 15:31:02
Job time: 293 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:30:44 ; Search time 11.63 Seconds
(without alignments)

680.963 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVHIVTKVEKVA.....LRVNQTFNWNNTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues 100059

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	1	CD80_HUMAN
2	738	64.2	299	1	CD80_RABIT
3	561	48.8	306	1	CD80_MOUSE
4	182	15.8	329	1	CD86_HUMAN
5	161	14.0	302	1	ICOL_HUMAN
6	152	13.2	309	1	CD86_MOUSE
7	150.5	13.1	322	1	ICOL_MOUSE
8	140.5	12.2	330	1	CD86_RABIT
9	134.5	11.7	583	1	C166_MOUSE
10	133.5	11.6	583	1	C166_HUMAN
11	129	11.2	221	1	BRF1_EBV
12	127	11.1	526	1	BUTY_HUMAN
13	122.5	10.7	588	1	C166_CHICK
14	119	10.4	524	1	BUTY_MOUSE
15	116.5	10.1	1088	1	NCA1_XENLA
16	115	10.0	761	1	NCA2_HUMAN
17	115	10.0	848	1	NCA1_HUMAN
18	110.5	9.6	321	1	TCB_FLY
19	109.5	9.5	646	1	MU18_HUMAN
20	109.5	9.5	853	1	NCA1_BOVIN
21	109	9.5	526	1	BUTY_BOVIN
22	109	9.5	2029	1	LAR_DROME
23	108.5	9.4	365	1	CXAR_MOUSE
24	106.5	9.3	333	1	AMAL_DROME
25	106.5	9.3	858	1	NCA1_RAT
26	105	9.1	319	1	A33_HUMAN
27	105	9.1	1091	1	NCA1_CHICK
28	104	9.1	1092	1	NCA2_XENLA
29	103.5	9.0	725	1	NCA2_MOUSE
30	103.5	9.0	1115	1	NCA1_MOUSE
31	103	9.0	298	1	VEJA_HUMAN
32	102	8.9	1443	1	NEO1_CHICK
33	101.5	8.8	403	1	RAGE_MOUSE

RESULT 1

ID	CD80_HUMAN	STANDARD:	PRT:	288 AA.
AC	P33681			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1 ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.1) (B7) (BB1).			
GN	CD80 OR CD28LG1 OR CD28LG OR LAB7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymphoid;			
RX	MEDLINE=90010147; PubMed=2794510;			
RA	Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F., Nadler L.M.;			
RA	"B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells.";			
RT	J. Immunol. 143:2714-2722(1989).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=92307753; PubMed=1377173;			
RX	Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.;			
RA	"Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7.";			
RT	Immunogenetics 36:173-181(1992).			
RL	[3]			
RP	SEQUENCE OF 35-38.			
RX	MEDLINE=91341422; PubMed=1714935;			
RA	Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;			
RT	"Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7.";			
RL	J. Exp. Med. 174:625-631(1991).			
RN	[4]			
RP	CHARACTERIZATION.			
RX	MEDLINE=95088403; PubMed=7527824;			
RA	Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;			
RT	"CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL.";			
RL	J. Immunol. 154:97-105(1995).			
CC	!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.			
CC	!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES AND DENDRITIC CELLS.			
CC	!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.			

34	100	8.7	413	1	HEMO_MANSE	P31398	manduca sex
35	99.5	8.7	1338	1	VGR1_HUMAN	P17948	homo sapien
36	98.5	8.6	365	1	CXAR_HUMAN	P78310	homo sapien
37	98	8.5	278	1	OX2G_RAT	P04218	rattus norv
38	98	8.5	298	1	JAM1_BOVIN	Q9xt56	bos taurus
39	98	8.5	1333	1	VGR1_MOUSE	P35969	mus musculus
40	97	8.4	1336	1	VGR1_RAT	P53767	rattus norv
41	96.5	8.4	739	1	VCA1_HUMAN	P19320	homo sapien
42	96	8.4	1020	1	CONT_MOUSE	P19600	mus musculus
43	95.5	8.3	811	1	FS22_DROME	P34083	drosophila
44	95.5	8.3	873	1	FS21_DROME	P34082	drosophila
45	95.5	8.3	1348	1	VGR2_COTJA	P52583	coturnix co

ALIGNMENTS

CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd80.htm".
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 CC EMBL; M27533; AAA36045.1; -;
 CC EMBL; M83077; AAA58390.1; -;
 CC EMBL; M83072; AAA58390.1; JOINED.
 CC EMBL; M83073; AAA58390.1; JOINED.
 CC EMBL; M83074; AAA58390.1; JOINED.
 CC PIR; A45803; A45803.1; JOINED.
 CC MIM; 112203; -;
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003600; Ig_Like.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00410; IG_Like; 1.
 CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 KW SIGNAL 1 34
 FT CHAIN 35 288
 FT DOMAIN 35 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 288
 FT DOMAIN 43 123
 FT DOMAIN 155 223
 FT DISULFID 150 116
 FT DISULFID 162 216
 FT CARBOHYD 53 53
 FT CARBOHYD 89 89
 FT CARBOHYD 98 98
 FT CARBOHYD 186 186
 FT CARBOHYD 207 207
 FT CARBOHYD 211 211
 FT CARBOHYD 226 226
 FT CARBOHYD 232 232
 FT CARBOHYD 288 AA; 33048 MW; BA453BE34528B1F4 CRC64;
 SQ SEQUENCE 288 AA; 33048 MW; BA453BE34528B1F4 CRC64;
 Query Match 100.0%; Score 1149; DB 1; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.6e-89;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGSDMNWPE 60
 Db 27 GLSHFCGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGSDMNWPE 86
 QY 61 YKNRTFTDITNLSIVILALRPDSDEGTCVVLKYEKDAFKREHLAEVTLVSKADPPTPS 120
 Db 87 YKNRTFTDITNLSIVILALRPDSDEGTCVVLKYEKDAFKREHLAEVTLVSKADPPTPS 146
 QY 121 ISDFEPTSNIRRIICSTSGGPPPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
 Db 147 ISDFEPTSNIRRIICSTSGGPPPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 206
 QY 181 NMTHNSFMCLIKYGLHRLVNTQFNNTTKQEHFPD 216
 Db 207 NMTHNSFMCLIKYGLHRLVNTQFNNTTKQEHFPD 242
 RESULT 2
 CD80_RABIT STANDARD; PRT; 299 AA.
 AC P42070;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1
 DE ANTIGEN).
 GN CD80.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHBB:HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules";
 RL Immunogenetics 42:217-220(1995).
 CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; D49843; BAA08643.1; -;
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003600; Ig_Like.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00410; IG_Like; 1.
 CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 KW SIGNAL 1 32
 FT CHAIN 33 299
 FT DOMAIN 33 243
 FT TRANSMEM 244 264
 FT DOMAIN 265 299
 FT DOMAIN 42 122
 FT DOMAIN 154 222
 FT DISULFID 49 115
 FT DISULFID 161 215
 FT CARBOHYD 52 52
 FT CARBOHYD 88 88
 FT CARBOHYD 97 97
 FT CARBOHYD 122 122
 FT CARBOHYD 185 185
 FT CARBOHYD 206 206
 FT CARBOHYD 210 210
 FT CARBOHYD 299 AA; 33513 MW; 6744223E5CC91DE0 CRC64;
 SQ SEQUENCE 299 AA; 33513 MW; 6744223E5CC91DE0 CRC64;
 Query Match 64.2%; Score 738; DB 1; Length 299;
 Best Local Similarity 63.9%; Pred. No. 8.9e-55;
 Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;
 QY 4 HFCSGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGSDMNWPEYKN 63
 Db 29 HFCSGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGSDMNWPEYKN 88
 QY 64 RTIFDITNLSIVILALRPDSDEGTCVVLKYEKDAFKREHLAEVTLVSKADPPTPSID 123
 Db 89 RTIFDITNLSIVILALRPDSDEGTCVVLKYEKDAFKREHLAEVTLVSKADPPTPSID 148
 QY 124 FEIPTSNIIRRIICSTSGGPPPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 183

Db 149 IGHDPNPVKIRCSASGPFPEPLAWMEDGEELNAVNTTVDQDLDTLYSVSSELDNVT 208
 QY 184 TNHSFMCILIKYHLRVNQFNWNTTQOE 211
 Db 209 NNHSIVCLIKYGLSVSIQFPWSPKQOE 236

RESULT 3
 CD80_MOUSE STANDARD; PRT; 306 AA.
 AC Q00609;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1
 DE ANTIGEN) (B7).
 GN CD80 OR B7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=91341422; PubMed=1714935;
 RA Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,
 RA White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
 RT "Structure, expression, and T cell costimulatory activity of the
 RT murine homologue of the human B lymphocyte activation antigen B7";
 RL J. Exp. Med. 174:625-631(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell.
 RX MEDLINE=93307789; PubMed=7686531;
 RA Selvakumar A., White P.C., Dupont B.;
 RT "Genomic organization of the mouse B-lymphocyte activation antigen
 RT B7";
 RL Immunogenetics 38:292-295(1993).
 CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
 CC INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
 CC MALIGNANCIES.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
 CC ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
 CC IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
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 DR EMBL; X60958; CAA43291.1; -;
 DR EMBL; L12589; AAA37240.1; ALT_SEQ.
 DR EMBL; L12585; AAA37240.1; JOINED.
 DR EMBL; L12586; AAA37240.1; JOINED.
 DR EMBL; L12587; AAA37240.1; JOINED.
 DR EMBL; L12588; AAA37240.1; JOINED.
 DR PIR; S17291; S17291.
 DR MGD; MGI:101775; Cd80.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 1.
 DR SMART; SM00410; IG_Like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 37
 FT CHAIN 38 306
 FT DOMAIN 38 246
 FT TRANSMEM 247 268
 FT DOMAIN 269 306
 FT DOMAIN 126 126
 FT DOMAIN 158 226
 FT DOMAIN 227 246
 FT DISULFID 54 119
 FT DISULFID 165 219
 FT CARBOHYD 93 93
 FT CARBOHYD 99 99
 FT CARBOHYD 149 149
 FT CARBOHYD 189 189
 FT CARBOHYD 210 210
 FT CARBOHYD 214 214
 SQ SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;

Query Match 48.8%; Score 561; DB 1; Length 306;
 Best Local Similarity 50.7%; Pred. No. 5.8e-40;
 Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTKEVEKATLSCGHNVSEELAQTRIYVQKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71
 Db 42 LSKSVKDKVLLPCRYNSPHEDESDRIYVQKHQKLVLSVIAAGLKVWPEYKNRTLYDNT- 100
 QY 72 NLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTSDPEIPTSNI 131
 Db 101 TSLIILGLVLSDRGTYSVQVQKRGTEYVKHLALVLSIKADFSFNPNTESGNPSADT 160
 QY 132 RRICSTSGGFPEPHLSWLENGELNAINVTSDPPELYAVSSKLDNFNTTNSHSEWCL 191
 Db 161 KRITCFASGFGFPKPRFSLWLENGELPGINTTISQDPSELYTISQDLDFNTRNHTIKCL 220
 QY 192 IKYGHRLRVNQTFFNWTNTKQEHFFDN 216
 Db 221 IKYGDARVSEDFTEWKPEDP-PDS 244

RESULT 4
 CD86_HUMAN STANDARD; PRT; 329 AA.
 AC P42081; Q13655;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
 DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (BU63).
 GN CD86 OR CD28LG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94053735; PubMed=7694363;
 RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
 RA Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.;
 RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
 RT cell proliferation";
 RL Science 262:909-911(1993).
 RN [2]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=94050123; PubMed=7694153;
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
 RA Lanier L.L., Somoza C.;
 RT "B70 antigen is a second ligand for CTLA-4 and CD28";
 RL Nature 366:76-79(1993).

CC -!- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S
 CC PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC -!- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOIESIS: IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC -!- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
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 CC -----
 CC EMBL; AF216747; AAF45149.1; -
 CC EMBL; AF199027; AAF34738.1; -
 CC EMBL; AX100591; CAC36463.1; -
 CC EMBL; AX100593; CAC36464.1; -
 CC EMBL; AF394451; AAK77544.1; -
 CC MGD; MGI:1354701; ICOS1.
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR003600; Ig_Like.
 CC Pfam: PF00047; Ig; 1.
 CC SMART; SM00410; IG_Like; 1.
 CC SMART; SM00410; IG_Like; 1.
 CC B-cell activation; Immune response; Glycoprotein;
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 KW Alternative splicing.
 FT SIGNAL 1 46 BY SIMILARITY.
 FT CHAIN 47 322 ICOS LIGAND.
 FT DOMAIN 47 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 298 POTENTIAL.
 FT DOMAIN 299 322 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 55 145 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 178 250 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 31 38 POLY-LEU.
 FT DOMAIN 289 292 POLY-ALA.
 FT DISULFID 62 138 POTENTIAL.
 FT CARBOHYD 185 243 POTENTIAL.
 FT CARBOHYD 120 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 321 322 HA -> TWAPVYQDYLIPYLSMSPCLKTRGLP (IN
 FT ISOFORM 2).
 FT CONFLICT 237 237 R -> H (IN REF. 4 AND 5; CAC36464).
 FT SEQUENCE 322 AA; 35960 MW; 55CCBA4AD12E47E6 CRC64;
 Query Match 13.1%; Score 150.5; DB 1; Length 322;
 Best Local Similarity 27.1%; Pred. No. 1.3e-05;
 Matches 65; Conservative 32; Mismatches 102; Indels 41; Gaps 12;
 QY 2 LSHFC--SGVIHTKVEKATSCGHNVSE-----ELAQTRIVYQWKEKKWV-----L 48
 Db 38 LSLCLASAEATGAMVGSNVVLSL-----IDPHRRHFNLSGLVYVQWIEPVSVTYYL 92
 QY 49 TMMSGDMNIWPEYKNTIFDITN-----NLSIVILALRPSDEGTVECVLVKEDAKFKEH 104

Db 93 PKSGINVDSSYKNGHLSLDSMKQGNPSLYLKNVTPDQTOFTCRV--FMTATELVK 150
 QY 105 LAE--VTLSVKADFTTP--SISDEIPTSNIIRICISTSGGPEPHLSWLENGEELNAIN 160
 Db 151 ILIEVVRLRAAFSTPVIKSTSSNPGQE-RYTTCKMSKNGYPEPNLYWI-NTDNLSD 208
 QY 161 TTVSODP---ETELVAVSSKLDENMTNHSFMCILKYGHLRVN-----OTFNNTTK 209
 Db 209 TALQNNVTYLNKGLDYLSTLRLPWTSRGDVLCCVENVALHQNITISQASFTGNNTK 268
 RESULT 8
 CD86_RABIT
 ID CD86_RABIT STANDARD; PRT; 330 AA.
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
 DE ANTIGEN).
 GN CD86.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHBB;HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules";
 RL Immunogenetics 42:217-220(1995).
 CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; D49842; BAA08642.1; -
 CC InterPro: IPR003006; Ig_MHC.
 CC SMART; IPR003596; Ig_V.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
 FT DOMAIN 23 247 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 248 268 POTENTIAL.
 FT DOMAIN 269 330 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 149 225 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 40 110 POTENTIAL.
 FT DISULFID 157 218 POTENTIAL.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 330 AA; 37142 MW; 935CDD65C57E3EE1 CRC64;

Query Match 12.2%; Score 140.5; DB 1; Length 330;
Best Local Similarity 27.4%; Pred. No. 9.4e-05;
Matches 60; Conservative 34; Mismatches 84; Indels 41; Gaps 12;

QY 18 EVATLSGCH-NVSEELAOPIRYWQEKKVLJMM-----SGDMNIPPEYKNRIFDITN- 71
Db 34 KTADLPQCFNSRSRSLVSELVWQDQRLVYELFLGKREKPNVDPKYIGRTSFQDES 93

QY 72 NLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLKADFPPTPSISDFEIPTSNI 131
Db 94 NLQHNVOIK--DKGVYQCFVHHRGAKGLVPIYQMNSLSVLNFATQPEIT-----LISNI 147

QY 132 RR-----IICSTGGPPEPHLSWLENGEELNAINTVV-----SQDPTELY--AVSS 176
Db 148 TRSAINLTCSSVOGYPEPKKMF-----VLKTENATTEYDGVIEKSDQNVNVTGLYNISIG 203

QY 177 KLDF-NMNTNHSFCLIKYGLHRLVNOTENWNTTKQEHFP 214
Db 204 SITFSDDIRNATYCVL-----QTESTETYSQ-HFP 233

RESULT 9
C166_MOUSE
ID C166_MOUSE STANDARD; PRT; 583 AA.
AC Q61490; 070136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE)
DE (ALCAM) (DM-GRASP PROTEIN).
-OS ALCAM.
-OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-NFS;
RX MEDLINE=97353242; PubMed=9209500;
RA Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
RA Kobay J., Stirling G.C., Siadak A.W., Aruffo A.;
RT "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT conserved in different homologs and mediates cross-species binding.";
RL Eur. J. Immunol. 27:1469-1478(1997).
RN [2]
RN SEQUENCE OF 227-583 FROM N.A.
RP STRAIN=BAIB/C; TISSUE=Brain;
RX MEDLINE=94376084; PubMed=8089660;
RA Kanki J.P., Chang S., Kuwada J.Y.;
RT "The molecular cloning and characterization of potential chick
RT DM-GRASP homologs in zebrafish and mouse.";
RL J. Neurobiol. 25:831-845(1994).
CC -!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC THE NERVOUS SYSTEM.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC 3 C2-LIKE AND 2 V-LIKE DOMAINS.
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CC EMBL; U95030; AAC06342.1; -.
CC DR EMBL; L25274; AAA37528.1; -.
CC DR MGI; L1313266; Alcam.
CC DR InterPro; IPR003599; Ig.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003600; Ig_like.
CC DR Pfam; PF00047; ig; 5
CC DR SMART; SM00409; IG; 3.
CC DR SMART; SM00410; IG_like; 2.
CC DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 583 CD166 ANTIGEN.
FT DOMAIN 28 527 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 528 549 POTENTIAL.
FT DOMAIN 550 583 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 263 321 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 347 399 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 428 492 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFID 43 113 POTENTIAL.
FT DISULFID 157 220 POTENTIAL.
FT DISULFID 270 313 POTENTIAL.
FT DISULFID 354 392 POTENTIAL.
FT DISULFID 435 485 POTENTIAL.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 227 232 PSQKT -> AAGIPA (IN REF. 2).
FT CONFLICT 454 454 S -> F (IN REF. 2).
SQ SEQUENCE 583 AA; 65161 MW; E7BFAF8FCA8F9489 CRC64;

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Query Match 11.7%; Score 134.5; DB 1; Length 583;
Best Local Similarity 25.2%; Pred. No. 0.00061;
Matches 38; Conservative 34; Mismatches 54; Indels 25; Gaps 7;

QY 59 PEYKNRTIFDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLKADFPPT 118
Db 84 PEYKDR--LSSLSENYTLSTANAKISDEKRFVCLVLT-EDNVFEAPTLVKV-----FKQ 133

QY 119 PSISDFE-----IPTSNIRRI-ICSTGGPPEPHLSWLENGEELNAINTVV-----QD 166
Db 134 PSKPEIVNKAPFLETDLKKGDCISRDSYPDGNITWRNGKVLQPVGEVAILFKKEID 193

QY 167 PETELYAVSSKLDNFNMTNH---SFMCLIKY 194
Db 194 PGTQLTYVTSSLEYKTRSDIQMPFTCSVTY 224

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RESULT 10
C166_HUMAN
ID C166_HUMAN STANDARD; PRT; 583 AA.
AC Q13740; O60892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE)
DE (ALCAM).
GN ALCAM OR MEMD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.

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CC -----
 DR EMBL; V01555; CAA24809.1; -
 DR PIR; A03792; Q0BE48.
 DR PIR; S33058; S33058.
 DR InterPro; IPR003600; Ig_like.
 DR SMART; SM00410; IG_like; 1.
 KW Early protein; Transforming protein.
 SQ SEQUENCE 221 AA; 24471 MW; CA5A24DLEA28758E CRC64;

Query Match 11.2%; Score 129; DB 1; Length 221;
 Best Local Similarity 27.0%; Pred. No. 0.00052;
 Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;

QY 18 EVATLSCGHNVSEELAQTRIVYQK-----EKKVLTMMSGDMNIWPE 60

DB 19 QAVTAFGLGERVLT-----YWRVSLGPEIEVSWFKLGPGEQVLIGRMHHDV-IFIE 71

QY 61 YKNTIFDI---TNLISIVILALRPSDEGTGECVWLKYEKDAFKREHLAEV---TLSV-- 112

DB 72 WPFGRGFDIHRSAFTFLVVTAAINSHDGNLGRMKLGETEVTQKHELNVVPLTSLVHS 131

QY 113 -KADFTPSISDEIFTSNRRICSTSGGFPPEHLSWL 150

DB 132 ERSQFP-----DFSILT-----VTCTVNAFPPHVQWL 159

RESULT 12

BUTY_HUMAN
 ID BUTY_HUMAN STANDARD; PRT; 526 AA.
 AC Q13410;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE BUTYROPHILIN PRECURSOR (BT).
 GN BTNL1 OR BTN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 RX MEDLINE=96201696; PubMed=8611614;
 RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
 RT "Cloning and sequence analysis of human butyrophilin reveals a
 potential receptor function."
 RL Biochim. Biophys. Acta 1306:1-4(1996).
 CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
 CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
 CC MEMBRANE (BY SIMILARITY).
 CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
 CC (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 1
 CC V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
 CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).

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CC -----
 DR EMBL; U39576; AAC50489.1; -
 DR MIM; 601610; -
 DR InterPro; IPR003879; Butyroph_DUF_C.
 DR InterPro; IPR001870; Gamma_carboxylase.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR003877; SPRY.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00622; SPRY; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00449; SPRY; 1.
 KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 526
 FT DOMAIN 27 242
 FT TRANSMEM 243 269
 FT DOMAIN 270 526
 FT CARBOHYD 55 55
 FT CARBOHYD 215 215
 SQ SEQUENCE 526 AA; 59004 MW; E9EAC0CF8DAF94D5 CRC64;

Query Match 11.1%; Score 127; DB 1; Length 526;
 Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

QY 16 VKEVATLSC--GHNVSVEELAQTRIVYQKKEKVMVLTMMSG---DMNIWPEYKNRTIF--- 67

DB 42 VGEDAELPCRLSPNASEHL-ELRWFKKVSPAVLVHRDGRGEAEQMEYVGRATLVQD 100

QY 68 -DITNLSIVILALRPSDEGTGECVWLKYEKDAFKREHLAEVTLVKADFTPTSDFEI 126

DB 101 GIAGRVVALRIGRVSDDDGEYTCF---FREDGSYEAL--VHLKVAALGSDPHIS-MQV 154

QY 127 PTSNIRRIICSTSGGFPPEHLSW--LENELNAINITVSODPETE--LYAVSSKLDENMTT 184

DB 155 QENGEICLECTSVGWYPEQVQVORTSGKEFP--SISESRNPDEEGLFTVAASVILRDT 212

QY 185 NHSFMCILIK 193

DB 213 TRNVSCIYQ 221

RESULT 13

C166.CHICK
 ID C166.CHICK STANDARD; PRT; 588 AA.
 AC P42292;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CD166 ANTIGEN PRECURSOR (SCI GLYCOPROTEIN) (BEN GLYCOPROTEIN) (DM-
 DE GRASP PROTEIN) (JC7 PROTEIN).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
 RC TISSUE=Embryo;
 RX MEDLINE=92030150; PubMed=1931049;

RA Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
 RA McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;

RT "Molecular cloning and expression of a novel adhesion molecule, SCI.;"
 RL Neuron 7:535-545(1991).

RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=91337449; PubMed=1873027;

RA Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
 RA Chang S.;

RT "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
 that supports neurite extension.;"

RL Neuron 7:209-220(1991).

RN [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.

RC TISSUE=Bursa of fabricius;

RX MEDLINE=92302224; PubMed=1608932;


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CC -----AAB51034.1; -
DR EMBL; U67065; AAB51034.1; -
DR EMBL; S80642; AAB35893.1; -
DR MGI; 103118; Btln1a1.
DR InterPro; IPR003879; Butyroph_c.
DR InterPro; IPR001870; Gamma_carboxylase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR003877; SPRY.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00449; SPRY; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 26
FT CHAIN 27 524
FT DOMAIN 27 247 BUTYROPHILIN.
FT TRANSMEM 248 268 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 269 524 POTENTIAL.
FT CARBOHYD 56 56 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 46 46 D -> DD (IN REF. 2).
FT CONFLICT 117 117 V -> F (IN REF. 2).
FT CONFLICT 191 191 E -> D (IN REF. 2).
FT CONFLICT 210 210 R -> S (IN REF. 2).
FT CONFLICT 363 363 V -> E (IN REF. 2).
FT CONFLICT 408 408 T -> K (IN REF. 2).
FT CONFLICT 413 414 SL -> FF (IN REF. 2).
FT CONFLICT 420 423 PRPV -> LAEY (IN REF. 2).
FT CONFLICT 492 509 DIPLSPLEGCTSGDKDT -> GHSLVPAGGRLYFWRQH
      (IN REF. 2).
FT SEQUENCE 524 AA; 58406 MW; 333F4DE2C7704480 CRC64;

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Query Match 10.4%; Score 119; DB 1; Length 524;
Best Local Similarity 23.8%; Pred. No. 0.011;
Matches 44; Conservative 34; Mismatches 87; Indels 20; Gaps 7;

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QY 20 ATLSGCH--NVSEELAQTRIVQKKEKVVLTMMSGD-----MNIWPEYKNR----TIFD 68
Db 47 AETCTGFSNASSEYM---ELLWFRQTRVALLYRDGQEQGQMTQTEYRGRATLATAGL 103
QY 69 ITNLSIVILALRPSDEGTVECVLVKYEADKREHLAEVTLVSKADFTPTPSIDFEIPT 128
Db 104 LDGRATLLIRDVRVSDGQYRC--LFKNDDEE---AAVYLKVAAGSDPQLS-MTVQE 157
QY 129 SNIRRICTSGGPPPHLSWLENGELNAINITVSDPETELIYAVSSKLDFTNMTNHSF 188
Db 158 NGEMELECTSSGWPBPQVQWRGTGNREMLPSTSESKKHNEGLFTVAVSMIRDSIKNM 217
QY 189 MGLIK 193
Db 218 SCIQ 222

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RESULT 15
NCAL_XENLA STANDARD; PRT; 1088 AA.
AC P16170.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180)
[CONTAINS: N-CAM 140].
GN NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_taxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90698871; PubMed=2481269;

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RA Krieg P.A., Sakaguchi D.S., Kintner C.R.;
FT "Primary structure and developmental expression of a large
FT cytoplasmic domain form of Xenopus laevis neural cell adhesion
FT molecule (NCAM).";
RL Nucleic Acids Res. 17:10321-10335(1989).
CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC NEURITES, ETC.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
CC TISSUE.
CC -1- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC EARLY NEURAL DEVELOPMENT.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M25696; AAA49909.1; -
DR FIR; S05600; IOLNLM.
DR HSSP; P56276; ITLK.
DR InterPro; IPR001777; FN_III.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1088
FT DOMAIN 20 705 NEURAL CELL ADHESION MOLECULE 1, LARGE
FT TRANSMEM 706 723 ISOFORM.
FT DOMAIN 724 1088 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 34 100 POTENTIAL.
FT DOMAIN 129 193 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 225 289 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 316 386 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 413 480 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 512 589 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 618 686 FIBRONECTIN TYPE-III 1.
FT DOMAIN 149 153 FIBRONECTIN TYPE-III 2.
FT DOMAIN 158 162 HEPARIN-BINDING (POTENTIAL).
FT DISULFID 41 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 282 PROBABLE.
FT DISULFID 323 379 PROBABLE.
FT DISULFID 420 473 PROBABLE.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 472 472 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 804 1049 MISSING (IN ISOFORM N-CAM 140).
SQ SEQUENCE 1088 AA; 117778 MW; 62738B5B03F3E83 CRC64;

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Query Match 10.1%; Score 116.5; DB 1; Length 1088;
Best Local Similarity 24.0%; Pred. No. 0.042;
Matches 43; Conservative 31; Mismatches 58; Indels 47; Gaps 9;

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Qy	18	EVALTSCGHNVSEELAQTRIYQWKEKKMWLTMMSGDMNIWPENKRTIFDITNLSIVI	77
- Db	130	EDAVIICDVSSPSI-----ITWRHGKDKVI-----FKKDVRFFVVLANNYLQI	173
Qy	78	LALRPSDEGYECVVLYEKDAKFREHLAEVTLVKADFPFISIDFEI---PTSNIIR-	133
Db	174	RGIKKTDEGTYRC-----EGRILARGEINYKDIOVTNPV-PTIQARQLRVNATANMAES	227
Qy	134	-IICTSGGPPEPLHSLWNGEELNAINTVSDPETELYAYSSKLDE-----MTTHH	186
Db	228	VVLSCDAGDFDPISLWKKGIEI-----EDGE-----EKLSIPNQOSEMTEIHH	271

Search completed: April 24, 2002, 15:33:55
Job time: 191 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:30:24 ; Search time 23.39 Seconds
(without alignments)
1350.783 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCSGVHVTKVEKVA.....LRVNOTFNWTKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	97.3	288	6	O77684
2	1100	95.7	288	6	O28499
3	1085	94.4	288	6	O9BDN6
4	1085	94.4	289	6	O28347
5	764	66.5	230	6	O9N213
6	762.5	66.4	288	6	O9TT70
7	762.5	66.4	297	6	O9BE99
8	761	66.2	229	6	O9TT71
9	743	64.7	292	6	O02758
10	743	64.7	292	6	O9GMZ8
11	719	62.6	304	6	O9TQX1
12	717.5	62.4	296	6	O46405
13	705	61.4	235	6	O9TQ58
14	705	61.4	235	6	O9N0T0
15	603.5	52.5	321	11	O35187
16	602	52.4	290	11	O62680
17	601.5	52.3	321	11	O62624
18	596	51.9	321	11	O55202
19	560	48.7	306	11	O9R129

20 350 30.5 174 6 O9GMZ9
21 255.5 22.2 212 11 O61332
22 200.5 17.4 329 6 O9XSX6
23 200.5 17.4 332 6 O9GMZ7
24 188.5 16.4 280 6 O9TTF1
25 188.5 16.4 296 13 O42404
26 182 15.8 329 6 O9TTF2
27 178 15.5 323 6 O9BDM2
28 177 15.4 323 6 O9BDM9
29 177 15.4 323 6 O9BDM4
30 176 15.3 275 6 O9BDN9
31 176 15.3 323 6 O9BDN8
32 171 14.9 284 6 O9GL33
33 162 14.1 313 11 O35531
34 161.5 14.1 325 6 O02838
35 161 14.0 302 4 O9HD18
36 161 14.0 309 4 O9NRQ1
37 156.5 13.6 290 4 O9NZQ7
38 153 13.3 290 11 O9EP73
39 153 13.3 356 11 O64381
40 152 13.2 314 11 O61238
41 150.5 13.1 322 11 O9JHJ8
42 142 12.4 316 4 O9BXRI
43 139.5 12.1 521 6 O46651
44 138 12.0 509 11 P97710
45 137 11.9 509 11 O9QWI5

ALIGNMENTS

RESULT 1

ID O77684 PRELIMINARY; PRT; 288 AA.
AC O77684;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE B7 PROTEIN.
GN B7.

OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.

RA Kraus G., Hnatyszyn J.H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
CC EMBL: AF079519; AAC31555.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00410; IG-like; 1.
SQ SEQUENCE 288 AA; 33131 MW; 76BBC42839E9AB79 CRC64;

Query Match 97.3%; Score 1118; DB 6; Length 288;
Best Local Similarity 97.7%; Pred. No. 3.3e-93;
Matches 210; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 LSHFCSGVHVTKVEKVAATLSGHNVSVEELAQTRYWQKEKKMVLTMSSGDMNWLPEY 61
DB 28 LSHFCSGVHVTKVEKVAATLSGHNVSVEELAQTRYWQKEKKMVLTMSSGDMNWLPEY 87
OY 62 KNTIFDITNNLSIVILALRPSDEGTYECVVKYKDAFKREHLAEVTLVKADFTTPI 121
DB 88 KNTIFDITNNLSIVILALRPSDEGTYECVVKYKDAFKREHLAEVTLVKADFTTPI 147

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QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLNENALNTTVSQDPETELYAVSSKLDNF 181
Db 148 TDFEIPPSNIRRIICSTSGGFPPEHLNENALNTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCILIKYGLRVNQTENNNTTKQEHFPDN 216
Db 208 MTNHSFMCILIKYGLRVNQTENNNTTKQEHFPDN 242

RESULT 2
ID Q28499 PRELIMINARY; PRT; 288 AA.
AC Q28499;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE B7 PROTEIN (CD80 PROTEIN PRECURSOR).
GN B7 OR N939.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=96003435; PubMed=7561102;
RA Villingier F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL Immunogenetics 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Villingier F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; U19840; AAA86706.1; -.
DR EMBL; AF344849; AAK37609.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_Like; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match 95.7%; Score 1100; DB 6; Length 288;
Best Local Similarity 96.3%; Pred. No. 1.4e-91;
Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIYQKKEKVMVLTMMSGDMNIWPEY 61
Db 28 LSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIYQKKEKVMVLTMMSGDMNIWPEY 87

QY 62 KNTIFDTNNLSIVILALRPSDEGTYECVVLKYEDAFKREHLAEVTLVSKADFTPSI 121
Db 88 KNTIFDTNNLSIVILALRPSDEGTYECVVLKYEDAFKREHLAEVTLVSKADFTPSI 147

QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLNENALNTTVSQDPETELYAVSSKLDNF 181
Db 148 TDFEIPPSNIRRIICSTSGGFPPEHLNENALNTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCILIKYGLRVNQTENNNTTKQEHFPDN 216
Db 208 MTNHSFMCILIKYGLRVNQTENNNTTKQEHFPDN 242

RESULT 4
ID Q28347 PRELIMINARY; PRT; 289 AA.
AC Q28347;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE B7 PROTEIN (FRAGMENT).
GN B7.
OS Cercopithecus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=96003435; PubMed=7561102;
RA Villingier F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; U19833; AAA86700.1; -.
DR InterPro; IPR003600; Ig_Like.

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RESULT 3
ID Q9BDN6 PRELIMINARY; PRT; 288 AA.
AC Q9BDN6;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CD80 PROTEIN.
GN MNB71.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA Villingier F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF344839; AAK37535.1; -.
SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;
Best Local Similarity 95.3%; Pred. No. 3.2e-90;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIYQKKEKVMVLTMMSGDMNIWPEY 61
Db 28 LSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIYQKKEKVMVLTMMSGDMNIWPEY 87

QY 62 KNTIFDTNNLSIVILALRPSDEGTYECVVLKYEDAFKREHLAEVTLVSKADFTPSI 121
Db 88 KNTIFDTNNLSIVILALRPSDEGTYECVVLKYEDAFKREHLAEVTLVSKADFTPSI 147

QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLNENALNTTVSQDPETELYAVSSKLDNF 181
Db 148 TDFEIPPSNIRRIICSTSGGFPPEHLNENALNTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCILIKYGLRVNQTENNNTTKQEHFPDN 216
Db 208 MTNHSFMCILIKYGLRVNQTENNNTTKQEHFPDN 242

RESULT 4
ID Q28347 PRELIMINARY; PRT; 289 AA.
AC Q28347;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE B7 PROTEIN (FRAGMENT).
GN B7.
OS Cercopithecus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=96003435; PubMed=7561102;
RA Villingier F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; U19833; AAA86700.1; -.
DR InterPro; IPR003600; Ig_Like.

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[illegible]

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CD80 PROTEIN PRECURSOR.
GN CD80/B7-1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LANDRACE; TISSUE=ILEUM MUCOSA;
RA Wada M., Amoe S., Sano N., Ishii T., Hoshi M., Sasaki H., Nio M.,
RA Hayashi Y., Ohi R.;
RT "cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble
RT isoforms.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RW EMBL; AB049760; BAB40952.1; -
KW SIGNAL.
DR CHAIN 1 29 POTENTIAL.
FT SIGNAL 30 297 CD80 PROTEIN.
SQ SEQUENCE 297 AA; 33438 MW; 23109711EA63EF23 CRC64;
Query Match 66.4%; Score 762.5; DB 6; Length 297;
Best Local Similarity 66.5%; Pred. No. 4.6e-61;
Matches 141; Conservative 28; Mismatches 42; Indels 1; Gaps 1;
QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQRIYWKKEKMKVLTMMSGDMNIWPE 60
DB 22 GLDFDCSGIVQVTKYKEIAVLSCDYNISTEELTRVRIYWKDNEMVLAVMSGKVKVWPK 81
QY 61 YKNTFTDITNNLSIVILALRPSDECTYECVVLKYKDAFKREHLAEVLSVKADFPPTS 120
DB 82 YENRTFTDVTNNLCIVILALRSLDNGTYTCVQKRGSGYKLEHLTSVKLMVKADFPVPS 141
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNATNTVSDPETELYAVSSKLD 180
DB 142 ITALGNPSPNIRKIRCTSGGPEPHLSWLENGEELNATNTVSDPETELYAVSSKLD 201
QY 181 NMTNHSFMCILIKYHLRVNQTFNW-NTTKQE 211
DB 202 NVTGNHSMCLVKYGLTVSQTFFNWQSAKRE 233
RESULT 8
Q9TT71 ID Q9TT71 PRELIMINARY; PRT; 229 AA.
AC Q9TT71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CD80 PROTEIN PRECURSOR.
GN CD80 OR CD80/B7-1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RA Fodor W.L., Meuller J.P., Matlis L.A., Rother R.P.;
RT "Primary Structure and Functional Characterization of a Soluble,
RT Alternatively Spliced Form of B7-1.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN.
RA Wada M., Amoe S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H.,
RA Ohi R.;
RT "Splicing Isoform of Porcine CD80.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DE EMBL; AF203442; AAF22749.1; -.

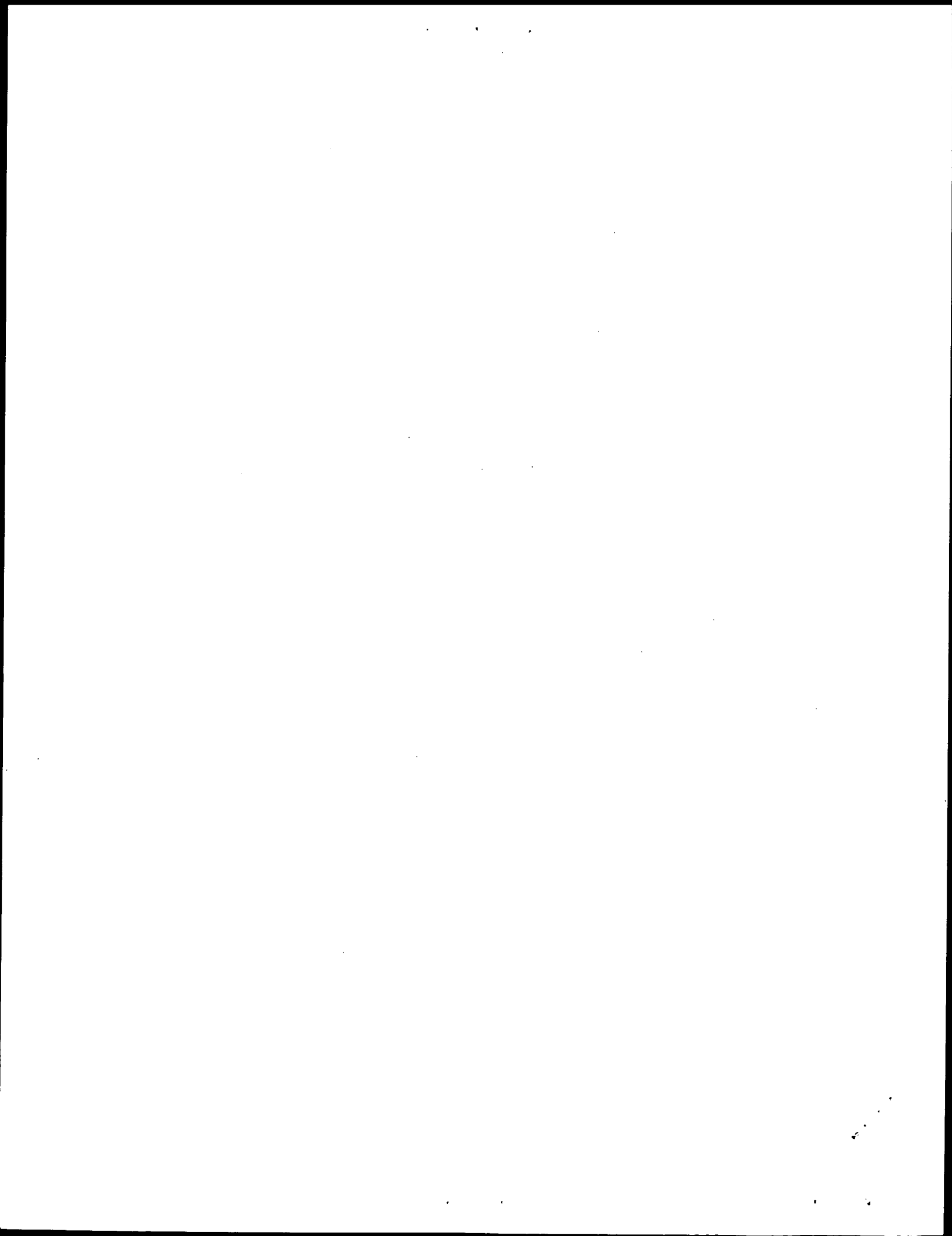
DR EMBL; AB038153; BAA90764.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_like; 1.
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 229 CD80 PROTEIN.
SQ SEQUENCE 229 AA; 25900 MW; C3AD172663C4A4ED CRC64;
Query Match 66.2%; Score 761; DB 6; Length 229;
Best Local Similarity 67.8%; Pred. No. 4.5e-61;
Matches 139; Conservative 26; Mismatches 40; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQRIYWKKEKMKVLTMMSGDMNIWPE 60
DB 22 GLDFDCSGIVQVTKYKEIAVLSCDYNISTEELTRVRIYWKDNEMVLAVMSGKVKVWPK 81
QY 61 YKNTFTDITNNLSIVILALRPSDECTYECVVLKYKDAFKREHLAEVLSVKADFPPTS 120
DB 82 YENRTFTDVTNNLCIVILALRSLDNGTYTCVQKRGSGYKLEHLTSVKLMVKADFPVPS 141
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNATNTVSDPETELYAVSSKLD 180
DB 142 ITALGNPSPNIRKIRCTSGGPEPHLSWLENGEELNATNTVSDPETELYAVSSKLD 201
QY 181 NMTNHSFMCILIKYHLRVNQTFNW 205
DB 202 NVTGNHSMCLVKYGLTVSQTFFNW 226
RESULT 9
ID 002758 PRELIMINARY; PRT; 292 AA.
AC 002758;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN B7-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Hash S.W.;
RL Thesis (1996); Texas A&M University, USA.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; U57755; AAB53575.1; -
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00410; Ig_like; 2.
SQ SEQUENCE 292 AA; 33482 MW; 6F117E7852B7950F CRC64;
Query Match 64.7%; Score 743; DB 6; Length 292;
Best Local Similarity 63.3%; Pred. No. 2.6e-59;
Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;
QY 2 LSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQRIYWKKEKMKVLTMMSGDMNIWPE 61
DB 28 LFYFCGIIQVKNKTVVEAVVLSCDYNISTEELTRVRIYWKDNEMVLAVMSGKVKVWPK 87
QY 62 KNTFTDITNNLSIVILALRPSDECTYECVVLKYKDAFKREHLAEVLSVKADFPPTS 121
DB 88 KNTFTDITNNLSIVILALRSLDNGTYTCVQKRGSGYKLEHLTSVKLMVKADFPVPS 147
QY 122 SDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNATNTVSDPETELYAVSSKLD 181

Db 148 TDLGNPSHNIKRMICLTSGGFPKPHLSWLENEELNAINTVSQDPETELYTISSELDNF 207
QY 182 MTNHSFCLVKYGLHVLNQTENNNTTKQEHFPDN 216
Db 208 MTNHSFCLVKYGLHVLNQTENNNTTKQEHFPDN 240
RESULT 10
Q9GMZ8 PRELIMINARY; PRT; 292 AA.
AC Q9GMZ8; 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE B-LYMPHOCYTE ACTIVATION ANTIGEN B7-1 (CD80).
GN CD80.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of the cDNA encoding the feline B-
RT lymphocyte activation antigen B7-1 (CD80) homologues."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB030651; BAB11687.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_Like; 2.
DR SMART; SM00410; Ig_Like; 2.
SQ SEQUENCE 292 AA; 33540 MW; ED9ABECEL0D30401 CRC64;
Query Match 64.7%; Score 743; DB 6; Length 292;
Best Local Similarity 63.3%; Pred. No. 2.6e-59;
Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;
QY 2 LSHFCSGVHVTKEVAVLSCGHNVSVBELAQTRIYWOKEKKMVLTMMSGDMNIWPEY 61
Db 28 LFVFCGIIQVKNKTVKEVAVLSCGHNVSVBELAQTRIYWOKEKKMVLTMMSGDMNIWPEY 87
QY 62 KNRTIFDITNNLSIVLALRPSDEGYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 121
Db 88 KNRTIFDITNNLSIVLALRPSDEGYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 147
QY 122 SDFEIPSTNIRRICSTSGGFPKPHLSWLENEELNAINTVSQDPETELYTISSELDNF 181
Db 148 TDLGNPSHNIKRMICLTSGGFPKPHLSWLENEELNAINTVSQDPETELYTISSELDNF 207
QY 182 MTNHSFCLVKYGLHVLNQTENNNTTKQEHFPDN 216
Db 208 MTNHSFCLVKYGLHVLNQTENNNTTKQEHFPDN 240
RESULT 11
Q9QX1 PRELIMINARY; PRT; 304 AA.
AC Q9QX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE B7-1 PROTEIN PRECURSOR.
GN CD80.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT Molecules";
RL Immunogenetics 50:349-353(1999).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF106824; AAF17295.1; -.
DR EMBL; AF106833; AAF17293.1; -.
DR EMBL; AF106829; AAF17293.1; JOINED.
DR EMBL; AF106830; AAF17293.1; JOINED.
DR EMBL; AF106831; AAF17293.1; JOINED.
DR EMBL; AF106832; AAF17293.1; JOINED.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_Like; 1.
KW Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 304 B7-1 PROTEIN.
SQ SEQUENCE 304 AA; 34454 MW; 09E082F6BB0C94F CRC64;
Query Match 62.6%; Score 719; DB 6; Length 304;
Best Local Similarity 60.5%; Pred. No. 4e-57;
Matches 130; Conservative 36; Mismatches 49; Indels 0; Gaps 0;
QY 2 LSHFCSGVHVTKEVAVLSCGHNVSVBELAQTRIYWOKEKKMVLTMMSGDMNIWPEY 61
Db 28 LFVFCGIIQVKNKTVKEVAVLSCGHNVSVBELAQTRIYWOKEKKMVLTMMSGDMNIWPEY 87
QY 62 KNRTIFDITNNLSIVLALRPSDEGYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 121
Db 88 ENRTFADFTNNLSIVLALRPSDEGYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 147
QY 122 SDFEIPSTNIRRICSTSGGFPKPHLSWLENEELNAINTVSQDPETELYTISSELDNF 181
Db 148 TDLGNPSHNIKRMICLTSGGFPKPHLSWLENEELNAINTVSQDPETELYTISSELDNF 207
QY 182 MTNHSFCLVKYGLHVLNQTENNNTTKQEHFPDN 216
Db 208 ITSNSFVCLVKYGLHVLNQTENNNTTKQEHFPDN 242
RESULT 12
O46405 PRELIMINARY; PRT; 296 AA.
AC O46405;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CD80 ANITGEN PRECURSOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Parsons K.R., Howard C.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; Y09950; CAA71081.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.

[illegible]

T	01-JAN-1998	(TReMBLrel. 05, Created)
T	01-JAN-1998	(TReMBLrel. 05, Last sequence update)



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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:26:09 ; Search time 23.25 Seconds
(without alignments)
688.165 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSFCSGVHVITKEVKA.....LRVQTFNWNITKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
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13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	AA67989	Human B lymphocyte
2	1149	100.0	288	AAW38414	B7-1. Homo sapien
3	1149	100.0	288	AAW67804	Human B7 protein s
4	1149	100.0	288	AAW73640	Human B7-2 antigen
5	1149	100.0	288	AAW37087	Human B lymphocyte
6	1149	100.0	288	AAW99966	Human B7 protein.
7	1149	100.0	288	AAW44289	Human B7.1 co-stim
8	1149	100.0	288	AAW54920	Human B7.1 protein
9	1149	100.0	288	AAU05121	Colorectal tumour
10	1149	100.0	288	AAW19959	Human B lymphocyte
11	1149	100.0	473	AAW41415	Human B7.1-murine

12	1146	99.7	251	20	AAW90208	hb7.lglu-glu solub
13	1144	99.6	475	18	AAW38415	Soluble B7-1-Ig.
14	1143	99.5	488	20	AAW86004	Human B7-1.5n4.1 p
15	1143	99.5	488	20	AAW83836	Amino acid sequenc
16	1143	99.5	492	19	AAW42338	CD80-ig-alpha-tp f
17	1138	99.0	480	20	AAW90206	hb7.lfc soluble fu
18	1047	91.1	208	18	AAW35858	Human B7.1 for use
19	761	66.2	229	22	AAW97780	Soluble porcine B7
20	743	64.7	232	21	AAW32283	Feline CD80 (B7-1)
21	743	64.7	232	21	AAW32276	Cat CD80 (B7-1)-TA
22	739	64.3	292	21	AAW32284	Feline CD80 (B7-1)
23	739	64.3	292	21	AAW32277	Cat CD80 (B7-1)-S
24	719	62.6	304	20	AAW41075	Canine B7-1 protei
25	705	61.4	235	20	AAW41077	Canine B7-1s prote
26	561	48.8	306	16	AAW82893	Mouse B7-1 alterna
27	561	48.8	306	16	AAW67990	Murine B lymphocyt
28	561	48.8	306	22	AAW19960	Mouse B lymphocyte
29	558	48.6	306	20	AAW82892	Mouse B7-1 alterna
30	558	48.6	306	20	AAW67805	Mouse B7-2 antigen
31	558	48.6	306	20	AAW73641	Mouse B7-2 antigen
32	558	48.6	306	21	AAW37088	Murine B lymphocyt
33	558	48.6	306	21	AAW99967	Murine B7 protein.
34	349.5	30.4	173	20	AAW41082	Feline B7-1s prote
35	311	27.1	214	16	AAW82901	Mouse B7-1 (Igv-11
36	305	26.5	200	16	AAW82900	Mouse B7-1 (Igv-11
37	250.5	21.8	212	16	AAW82902	Mouse B7-1 Igv-lik
38	250.5	21.8	226	16	AAW82903	Mouse B7-1 Igv-lik
39	200.5	17.4	329	21	AAW32285	Feline CD86 (B7-2)
40	200.5	17.4	329	21	AAW32278	Cat CD86 (B7-2) 11
41	200.5	17.4	332	20	AAW41079	Feline B7-2 protei
42	188.5	16.4	280	20	AAW41078	Canine B7-2s prote
43	182	15.8	244	20	AAW90209	hb7.lhis soluble f
44	182	15.8	246	20	AAW86005	Human B7-2 extrac
45	182	15.8	246	22	AAW83837	Amino acid sequenc

ALIGNMENTS

RESULT 1

AAW67989	AAW67989 standard; Protein; 288 AA.
ID	AAW67989 standard; Protein; 288 AA.
XX	
AC	AAW67989;
DT	21-AUG-1995 (first entry)
XX	
DE	Human B lymphocyte antigen B7-1 (hb7-1).
XX	
KW	B lymphocyte antigen; B7-1; B cell activation antigen; CD28;
KW	ligand; T cell surface antigen; transmembrane protein.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	1..34
FT	/label= signal sequence
FT	/note= "hydrophobic"
FT	35..242
FT	/label= extracellular
FT	243..269
FT	/label= transmembrane
FT	270..288
FT	/label= intracellular
FT	53..55
FT	/label= N-linked glycosylation
FT	89..91
FT	/label= see above
FT	98..100
FT	/label= see above
FT	186..188
FT	/label= see above
FT	207..209

FT Misc-difference 211...213 /label= see above
 FT FT Misc-difference 226...228 /label= see above
 FT FT Misc-difference 232...234 /label= see above
 FT FT Domain 35...138 /label= see above
 FT FT Domain 139...236 /label= Ig V-set domain
 FT FT Domain 139...236 /label= Ig C-set domain
 XX XX WO9503408-A.
 PN 02-FEB-1995.
 PD 26-JUL-1994; 94WO-US08423.
 XX 26-JUL-1993; 93US-0101624.
 PR 19-AUG-1993; 93US-0109393.
 PR 03-NOV-1993; 93US-0147773.
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (REPK) REPLIGEN CORP.
 XX Freeman GJ, Gray GS, Greenfield E, Nadler LM;
 XX WPI; 1995-075236/10.
 DR N-PSDB; AAQ81371.
 XX Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
 PT for enhancing or suppressing T-cell mediated immune responses
 XX Disclosure; pages 111-113; 175pp; English.
 XX Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,
 CC cell line Raji, clone no. 13. Its position in the genome is
 CC chromosome/segment 3. It was published by Freeman, F.J. et al.,
 CC J. of Immunology, 143: 8: 2714-2722, 15th October 1989. It can be
 CC found in Genbank at Accession no. M27533. The encoded protein,
 CC R67989, binds both human CTLA4 and human CD28. It is related
 CC to human hb7-2 (see Q81351) and murine hb7 (see Q81372).
 XX SQ Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 16; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWOKEKMMVLTMMSGDMNIWPE 60
 Db 27 glshfcsgvihvtkevevatlscghnsvveelaqtriwqekkmvltmmsgdmniwpe 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLGVKADFPPTS 120
 Db 87 ykntifdntnlsivilalrpsdegyecvvlkyekdafkrehlaevtlsvkadtpts 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSDPETELYAVSSKLDF 180
 Db 147 isdfeltsnirriicstsggfppehlswnleengeelnaintvtsqdpetelyavssklidf 206
 QY 181 NMNTNHSFMCILIKYGHRLRVNQTFFNNTTKQEHFPDN 216
 Db 207 nmntnhsfmclikyghrlrvnqtfnnnttkqehfpdn 242
 RESULT 2
 AAW38414
 ID AAW38414 standard; Protein; 288 AA.
 XX AC
 XX AAW38414;
 XX

DT 08-APR-1998 (first entry)
 XX B7-1.
 DE Screening; inhibitor; enhancer; binding; CD28; B7-1.
 XX Screening; inhibitor; enhancer; binding; CD28; B7-1.
 KW Homo sapiens.
 OS EP795554-A2.
 PN 17-SEP-1997.
 PD 04-MAR-1997; 97EP-0301438.
 XX 02-OCT-1996; 96JP-0262085.
 PR 05-MAR-1996; 96JP-0047795.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA Hattori M, Hida T, Kurokawa T, Nakanishi A;
 PI WPI; 1997-450803/42.
 DR N-PSDB; AAT96358.
 XX New xanthene derivatives useful as immunomodulators - e.g. methyl
 PT 2-(carboxymethylsulphanyl)-5,7-dichloro-3,8-dihydroxy-6-
 PT methyl-9-oxo-9H-xanthene-1-carboxylate.
 XX Disclosure; Fig 4; 117pp; English.
 XX The present sequence was used in the development of a novel method
 CC for screening for compounds that inhibit or enhance binding of CD28
 CC to B7-1.
 XX SQ Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 18; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWOKEKMMVLTMMSGDMNIWPE 60
 Db 27 glshfcsgvihvtkevevatlscghnsvveelaqtriwqekkmvltmmsgdmniwpe 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLGVKADFPPTS 120
 Db 87 ykntifdntnlsivilalrpsdegyecvvlkyekdafkrehlaevtlsvkadtpts 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSDPETELYAVSSKLDF 180
 Db 147 isdfeltsnirriicstsggfppehlswnleengeelnaintvtsqdpetelyavssklidf 206
 QY 181 NMNTNHSFMCILIKYGHRLRVNQTFFNNTTKQEHFPDN 216
 Db 207 nmntnhsfmclikyghrlrvnqtfnnnttkqehfpdn 242
 RESULT 3
 AAW67804
 ID AAW67804 standard; Protein; 288 AA.
 XX AC
 XX AAW67804;
 XX 13-APR-1999 (first entry)
 DT Human B7 protein sequence.
 DE Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;
 KW T- cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
 XX OS
 XX Homo sapiens.
 XX

Db 87 yknrtifdtnslsvillalrpsdegtyecvvlkyekdafkrehlavtlsvkadftps 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNATNTVSQDPETELVAVSSKLD 180
 Db 147 isdfeiptsnirriicstsggfpephlswnleengeelnaintvsqdpetelyavsskl 206
 QY 181 NMTNHSFMCILIKYGLHVRNQTNNNTTKQEHFPDN 216
 Db 207 mntnhsfmcilikyghlrvnqtnwnttkqehfpdn 242

RESULT 5
 AAB37087
 ID AAB37087 standard; Protein; 288 AA.
 AC AAB37087;
 DT 28-MAR-2001 (first entry)
 XX Human B lymphocyte antigen B7-1.
 DE Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
 KW antigen; extracellular domain; CTLA4; immunoglobulin constant region;
 KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
 KW T cell-mediated immune response; transplantation; vaccination.
 XX Homo sapiens.
 OS US6130316-A.
 PN 10-OCT-2000.
 PD 26-JUL-1994; 94US-0280757.
 PR 26-JUL-1993; 93US-0101624.
 PR 19-AUG-1993; 93US-0109393.
 PR 03-NOV-1993; 93US-0147773.
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (REPK) REPLIGEN CORP.
 XX Freeman GJ, Nadler LM, Gray GS, Greenfield E;
 PI WPT; 2000-655681/63.
 DR N-PSDB; AAC84051.
 XX Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for
 enhancing or suppressing T cell-mediated immune responses, especially
 during tissue, skin or organ transplantation, or in graft-versus-host
 disease -
 XX Disclosure; Column 87-90; 83pp; English.

The invention relates to an isolated nucleic acid molecule encoding a
 fusion protein comprising a first nucleotide sequence encoding a first
 peptide, and a second nucleotide sequence encoding a second peptide.
 The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium
 citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C
 to a portion of a nucleotide sequence which encodes a human or murine
 B lymphocyte antigen (B7-2) extracellular domain. The first peptide has
 the ability to bind CD28 or CTLA4. The first peptide has an amino acid
 sequence that is identical or at least 50% identical with the
 extracellular domain of a human B7-2 peptide (AAB37085). The second
 peptide is especially an immunoglobulin constant region. This sequence
 represents the human B lymphocyte antigen B7-1. The sequence is used for
 comparison with the B7-2 sequence. The human B7-2 protein is an example
 of a first peptide sequence of the invention. The nucleic acid molecules
 are useful in various expression vectors to direct synthesis of the
 corresponding proteins or peptides in a variety of hosts, particularly
 eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic
 acids are also useful for enhancing the immunogenicity of a mammalian
 cell, e.g. tumour cell (sarcoma) or an antigen presenting cell

CC (macrophage). The fusion proteins or peptides are useful for enhancing or
 suppressing T cell-mediated immune responses, e.g. in situations of
 tissue, skin or organ transplantation, or in graft-versus-host disease.
 CC The proteins are also useful for enhancing the efficacy of vaccination
 against a variety of pathogens, and may also be used to upregulate an
 immune response against a particular pathogen during an infection or
 against a tumour in a tumour-bearing host.
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAOTRIYQKREKKVLLTMMSGDMNIWPE 60
 Db 27 glshfcsgvihvtkevkevatslscghnsvsveelaqtriyyqkrekkmvlmmsgdmniwpe 86
 QY 61 YKNRTIFDITNLSIVILLALRPSDEGTVECVVLKYEKDAFKREHLAEVTLVSKADFPPTS 120
 Db 87 yknrtifdtnslsvillalrpsdegtyecvvlkyekdafkrehlavtlsvkadftps 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNATNTVSQDPETELVAVSSKLD 180
 Db 147 isdfeiptsnirriicstsggfpephlswnleengeelnaintvsqdpetelyavsskl 206
 QY 181 NMTNHSFMCILIKYGLHVRNQTNNNTTKQEHFPDN 216
 Db 207 mntnhsfmcilikyghlrvnqtnwnttkqehfpdn 242

RESULT 6
 AAY99966
 ID AAY99966 standard; Protein; 288 AA.
 AC AAY99966;
 DT 10-JAN-2001 (first entry)
 XX Human B7 protein.
 KW B7; human; B cell activation antigen; B lymphocytes;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW herpes simplex; influenza; common cold; HIV.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..34
 FT Domain 35..242 /label= signal_peptide
 FT Domain 35..242 /label= Extracellular_domain
 FT Domain 35..138 /label= "Ig V-set domain"
 FT Modified-site 53..55 /note= "N-linked glycosylation site"
 FT Modified-site 89..91 /note= "N-linked glycosylation site"
 FT Modified-site 98..100 /note= "N-linked glycosylation site"
 FT Domain 139..236 /note= "N-linked glycosylation site"
 FT Modified-site 186..188 /label= "Ig C-set domain"
 FT Modified-site 207..209 /note= "N-linked glycosylation site"
 FT Modified-site 211..213 /note= "N-linked glycosylation site"
 FT Modified-site 226..228 /note= "N-linked glycosylation site"
 FT Modified-site 232..234 /note= "N-linked glycosylation site"
 FT Modified-site 232..234 /note= "N-linked glycosylation site"

FT Domain 243..269
 FT /label= Transmembrane_domain
 FT 270..288
 FT /label= Intracellular_domain
 XX
 PN US6071716-A.
 XX
 PD 06-JUN-2000.
 XX
 XX 15-NOV-1993; 93US-0153262.
 XX
 XX 28-AUG-1991; 91US-0751306.
 PR 01-OCT-1990; 90US-0591300.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 PA
 XX Nadler LM, Freeman GJ, Freedman AS;
 PI
 XX WPI: 2000-422081/36.
 DR N-PSDB; AAA61328.
 XX
 XX New polynucleotides encoding a B7 activation antigen, useful for
 PT regulating T cell mediated immune responses or viral diseases -
 PT
 PS Claim 1; Fig 4; 36pp; English.
 XX
 CC The present sequence is the unique human B cell activation antigen B7
 CC protein. The cDNA encoding this sequence was isolated from a Burkitt
 CC lymphoma cell line cDNA library. Selection of cDNA clones was based
 CC on expression of B7, as detected by the anti-B7 monoclonal antibody.
 CC The human B7 cDNA was used in hybridisation analysis to isolate the
 CC murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be
 CC used to generate transgenic, knock-out animals which, in turn, are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The expressed B7 protein is useful for enhancing or
 CC blocking activated T cell mediated immune responses and immune
 CC function. Modification of B7 expression is useful in the treatment of
 CC autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis),
 CC herpes simplex, influenza, the common cold and HIV. It is also useful
 CC in tissue and organ transplantation.
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVEKATLSCGHNVSVLELAQTRIYWKQKMKVLTMMSGDMNIWPE 60
 DB 27 glshfcsgvihvtkevkatlscghnvsvleelaqtri-ywkqkkmvltmmsgdmniwpe 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVSKADFTPTS 120
 DB 87 ykntifdiitnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadftpts 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVTSQDPETELYAVSSKLDIF 180
 DB 147 isdfeiptsnirriicstsggfppephlswlengeelnaaintvtsqdpetelyavssklidf 206
 QY 181 NMNTNHSFMCILIKYGHILRVNQTFNNTTKQEHFPDN 216
 DB 207 nmntnhsfmcilikyghilrvnqtfnwnttkqehfpdn 242

RESULT 7
 AAY44289
 ID AAY44289 standard; Protein: 288 AA.
 XX
 AC AAY44289;
 XX
 XX 29-FEB-2000 (first entry)
 DT
 XX

DE Human B7.1 co-stimulatory molecule.
 XX
 KW Human B7.1 co-stimulatory molecule; antigen presenting cell;
 KW immune response; cell surface receptor; Major histocompatibility complex;
 KW MHC classii; proton motor force; mitochondrial membrane potential;
 KW mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
 KW neurodegenerative disorder.
 XX
 OS Homo sapiens.
 PN WO9953953-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 30-MAR-1999; 99WO-US06874.
 PR 17-APR-1998; 98US-0082250.
 PR 29-JUL-1998; 98US-0094519.
 PR 24-SEP-1998; 98US-0101580.
 XX
 XX (UYVE-) UNIV VERMONT.
 PA
 XX Newell MK;
 PI
 XX WPI: 2000-096773/08.
 DR N-PSDB; AA229320.
 XX
 XX Use of cell surface and membrane characteristics for developing
 PT products for treating cancers, autoimmune diseases or neurodegenerative
 PT diseases -
 PT
 PS Disclosure; Page 115; 123pp; English.
 XX
 CC The present sequence is human B7.1 co-stimulatory molecule. This is
 CC a glycoprotein on the surface of antigen presenting cells. This is
 CC involved in stimulation of an immune response by its ability to interact
 CC with various immune cell surface receptors. The regulation of cell
 CC surface expression of MHC classii and co-stimulatory molecule B7 can be
 CC manipulated by regulating the intracellular dissipation of proton motor
 CC force which can be assessed in terms of mitochondrial membrane potential.
 CC These methods can be used for regulating cell growth and division to
 CC control disease processes by manipulating mitochondrial metabolism and
 CC the expression of cell surface immune proteins. They can be used for
 CC treating diseases associated with excessive cellular division, aberrant
 CC differentiation, and premature cellular death, e.g. cancers, autoimmune
 CC diseases, neurodegenerative disorders etc.
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVEKATLSCGHNVSVLELAQTRIYWKQKMKVLTMMSGDMNIWPE 60
 DB 27 glshfcsgvihvtkevkatlscghnvsvleelaqtri-ywkqkkmvltmmsgdmniwpe 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVSKADFTPTS 120
 DB 87 ykntifdiitnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadftpts 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVTSQDPETELYAVSSKLDIF 180
 DB 147 isdfeiptsnirriicstsggfppephlswlengeelnaaintvtsqdpetelyavssklidf 206
 QY 181 NMNTNHSFMCILIKYGHILRVNQTFNNTTKQEHFPDN 216
 DB 207 nmntnhsfmcilikyghilrvnqtfnwnttkqehfpdn 242

RESULT 8
 AAY54920

ID AAY54920 standard; Protein; 288 AA.
 AC AAY54920;
 XX
 DT 14-FEB-2000 (first entry)
 XX
 DE Human B7.1 protein sequence.
 XX
 KW Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
 KW IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.
 XX
 OS Homo sapiens.
 XX
 PN US5994104-A.
 XX
 PD 30-NOV-1999.
 XX
 PF 08-NOV-1996; 96US-0751767.
 XX
 PR 08-NOV-1996; 96US-0751767.
 XX
 PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
 XX
 PI Anderson RJ, Prentice HG, MacDonald ID;
 XX
 DR WPI; 2000-038261/03.
 DR N-PSDB; AAZ40022.
 XX
 PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful
 PT for treating leukemia and other cancers -
 XX
 PS Example; Fig 10; 73pp; English.
 CC
 CC This sequence represents the human B7.1 protein sequence.
 CC The invention relates to an isolated nucleic acid construct (I)
 CC comprising a region encoding an interleukin-12 (IL-12) fusion protein
 CC (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker
 CC peptide (joining the subunits)) and a region encoding a B7 protein. (I)
 CC may be used to produce IL-12 fusion proteins according to standard
 CC recombinant DNA methodologies. The fusion proteins may be produced either
 CC in vitro in a fermentation culture or in vivo as part of a gene therapy
 CC protocol (in this case (I) is used to transform a patients cells, which
 CC then secrete the functional polypeptide to supplement the patients own
 CC production of IL-12 or to rectify mutations which lead to the expression
 CC of inactive polypeptides). The fusion proteins produced in this way may
 CC be used to treat any disease which responds to IL-12 such as tumours
 CC (both solid and dispersed of the kidney, breast, colon, ovarian and
 CC cervical tumours and melanomas) and in particular, tumours of the blood
 CC such as leukaemia. Alternatively, the polypeptides may be used as
 CC antigens in the production of antibodies to IL-12 and to assay for
 CC agonists and antagonists of its activity. The antibodies and antagonists
 CC may be used to inhibit the activity of IL-12. (I) may also be used
 CC diagnostically as a probe which hybridizes to sequences encoding IL-12
 CC and the antibodies may be used to detect the presence of IL-12
 CC polypeptides in samples. They may be used diagnostically to quantitate
 CC the expression of the polypeptide by patients and hence which subjects
 CC may be in need of restorative therapy.
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLSHFCGVIHVTKEVATLSCGHNVSEELAQTRIYWQKEKRMVLTMMSGDMNIWPE 60
 DB 27 glshfcgvihtvkevatlschghnsvseelaqtriwyqekkmvltmmsgdmniwpe 86
 OY 63 YKNRTFTDITNNLSIVILALRPSDECTYECVVLKYKDAFKREHLAEVLSVKADPTPS 120
 DB 87 yknrtftdntnlsivilarpsdegtcevcvlikykdafkrehlaevlsvkadftpts 146

OY 121 ISDFEIPTSNIRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELVAVSSKLPF 180
 DB 147 Isdfeptrsnirriicstsggfpephlswnleengeelnaintvsqdpetelyavssklkf 206
 OY 181 NMTTNSFMCILKYGHLRVNQTFNWNNTKQEHFPDN 216
 DB 207 nmttnhsfmcilikyghlrvnqtfnwnntkqehfpdn 242
 RESULT 9
 AAU05121
 ID AAU05121 standard; Protein; 288 AA.
 XX
 AC AAU05121;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Colorectal tumour antigen CD80.
 XX
 KW Colorectal cancer; immunostimulant; cytostatic; immune response;
 KW adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cell;
 KW SW403 cell; colon; breast; lung; prostate; cancer; vaccine;
 KW tumour antigen CD80.
 XX
 OS Homo sapiens.
 XX
 PN WO200154716-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-US02731.
 XX
 PR 27-JAN-2000; 2000US-0178498.
 PR 28-FEB-2000; 2000US-0185335.
 XX
 PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;
 XX
 DR WPI; 2001-502616/55.
 DR N-PSDB; AAS11426.
 XX
 PT New composition comprising an allogeneic tumour cell, useful for
 PT stimulating an immune response in a patient having an adenocarcinoma,
 PT especially useful for treating colorectal, breast, lung or prostate
 PT cancer -
 XX
 PS Example 2; Page 130-131; 131pp; English.
 CC
 CC The invention relates to a composition for stimulating an immune response
 CC in a patient having an adenocarcinoma or colorectal cancer. The
 CC composition comprises an allogeneic tumour cell selected from SW620 cell,
 CC COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic
 CC cell stimulates an immune response to an autologous tumour cell in the
 CC patient. The composition is useful for stimulating an immune response in
 CC a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate
 CC adenocarcinoma. The use of allogeneic tumour cells provides a generic
 CC source of antigen that can be administered to a variety of patients, in
 CC contrast to using autologous tumour cells, which must be isolated from
 CC each individual patient. The allogeneic cells are suitable as a cancer
 CC vaccine and can stimulate an immune response against autologous tumour
 CC cells of a cancer patient. The present sequence represents the amino acid
 CC sequence of colorectal tumour antigen CD80 used in the method of the
 CC invention.
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 22; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVEFLAOTRIYQKEKKMVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVEFLAOTRIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLISKADFPPTPS 120
DB 87 YKNTIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLISKADFPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPPPEHLNLSWENGEELNAINTVSQDPETELYAVSSKLDLF 180
DB 147 ISDFEIPTSNIRRIICSTSGGPPPEHLNLSWENGEELNAINTVSQDPETELYAVSSKLDLF 206
QY 181 NMTTNHSEWCLIKYGLHVRNQTENNNTKOEHPFDN 216
DB 207 NMTTNHSEWCLIKYGLHVRNQTENNNTKOEHPFDN 242

RESULT 10
AAB19959
ID AAB19959 standard; Protein; 288 AA.
AC AAB19959;
XX
XX
XX 19-MAR-2001 (first entry)
XX Human B lymphocyte antigen B7.
DE
XX Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;
KW CD28; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
KW metastasis; antitumour; therapy.
XX
XX Homo sapiens.

Key Location/Qualifiers
FH Peptide 1..34
FT /label= Signal_peptide
FT Protein 35..288
FT /label= Mature_protein
FT Domain 35..242
FT /note= "extracellular domain"
FT Domain 243..269
FT /note= "transmembrane domain"
FT Domain 270..288
FT /note= "intracellular domain"
FT Domain 35..138
FT /note= "immunoglobulin V-set domain"
FT Domain 139..236
FT /note= "immunoglobulin C-set domain"
FT Modified-site 53..55
FT /note= "Asn is N-glycosylated"
FT Modified-site 89..91
FT /note= "Asn is N-glycosylated"
FT Modified-site 98..100
FT /note= "Asn is N-glycosylated"
FT Modified-site 186..188
FT /note= "Asn is N-glycosylated"
FT Modified-site 207..209
FT /note= "Asn is N-glycosylated"
FT Modified-site 211..213
FT /note= "Asn is N-glycosylated"
FT Modified-site 226..228
FT /note= "Asn is N-glycosylated"
FT Modified-site 232..234
FT /note= "Asn is N-glycosylated"

US6149905-A.
XX
XX 21-NOV-2000.
XX
XX 23-SEP-1998; 98US-0159135.
XX
XX 03-NOV-1993; 93US-0147772.
XX

PA (GEM) GENETICS INST INC.
PA (DAND) DANA FARBEN CANCER INST INC.
PA (HARD) HARVARD COLLEGE.
XX
PI Baskar S, Glimcher LH, Freeman GJ, Ostrand-Rosenberg S;
PI Nadler LM;
XX
XX WPI: 2001-079388/09.
DR N-PSDB; AAA89224.
XX
XX Modifying tumor cell for treating tumors, reducing metastatic spread,
PT inhibiting recurrence of tumor and increasing immunogenicity, involves
PT transfecting tumor cells with a nucleic acid encoding B7 molecule -
XX
XX Claim 4; Column 31-34; 24pp; English.
XX
XX The present sequence is that of human lymphocyte antigen B7, a T
CC cell costimulatory molecule that binds to CD28 and CTLA4. Tumour
CC cells modified to express a T cell costimulatory molecule,
CC especially B7, are disclosed. The tumour cells are modified by
CC transfection with a nucleic acid encoding the T cell costimulatory
CC molecule, by using an agent which induces or increases expression
CC of the T cell costimulatory molecule on the tumour cell surface, or
CC by coupling the T cell costimulatory molecule to the tumour cell
CC surface. Tumour cells further modified to express major
CC histocompatibility complex (MHC) class I and/or class II molecules,
CC or in which expression of an MHC associated protein, the invariant
CC chain, is inhibited are also disclosed. The modified tumour cells
CC are used to treat a patient with a tumour, preventing or inhibiting
CC metastatic spread or tumour recurrence. The tumour may be a
CC melanoma, a neuroblastoma, a leukaemia or a carcinoma. A method for
CC specifically inducing a CD4+ T cell response against a tumour, and a
CC method for treating a tumour by modification of tumour cells in vivo
CC are also disclosed. The treatment methods increase the immunogenicity
CC of the tumour cell in vivo. The antitumour T cell-mediated immune
CC response is effective both against the modified tumour cells and the
CC unmodified tumour cells from which the modified cells were derived.
CC Thus, the effector phase of the antitumour response induced by the
CC modified tumour cells is not dependent upon expression of a
CC costimulatory molecule on the tumour cells.
XX
SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 22; Length 288;
Best Local Similarity 100.0%; Pred. No. 2e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVEFLAOTRIYQKEKKMVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVEFLAOTRIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLISKADFPPTPS 120
DB 87 YKNTIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLISKADFPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPPPEHLNLSWENGEELNAINTVSQDPETELYAVSSKLDLF 180
DB 147 ISDFEIPTSNIRRIICSTSGGPPPEHLNLSWENGEELNAINTVSQDPETELYAVSSKLDLF 206
QY 181 NMTTNHSEWCLIKYGLHVRNQTENNNTKOEHPFDN 216
DB 207 NMTTNHSEWCLIKYGLHVRNQTENNNTKOEHPFDN 242

RESULT 11
AAW41415
ID AAW41415 standard; Protein; 473 AA.
XX
XX AAW41415;
XX AC
XX XX
XX 02-JUN-1998 (first entry)
XX

Db 207 nmthshfmciklyghlrnvqtnfwnntkqghfpdn 242
|||||

RESULT 13

AAW38415
ID AAW38415 standard; Protein; 475 AA.

XX AC AAW38415;
XX 08-APR-1998 (first entry)
XX Soluble B7-1-Ig.
XX Screening; inhibitor; enhancer; binding; CD28; B7-1;
KW soluble B7-1-Ig; immunoglobulin.
XX Homo sapiens.

XX EP795554-A2.
XX 17-SEP-1997.

XX 04-MAR-1997; 97EP-0301438.
XX 02-OCT-1996; 96TP-0262085.
XX 05-MAR-1996; 96JP-0047795.

XX (TAKE) TAKEDA CHEM IND LTD.
XX Hattori M, Hida T, Kurokawa T, Nakanishi A;
XX WPI; 1997-450803/42.
XX N-PSDB; AAT96359.

XX New xanthene derivatives useful as immunomodulators - e.g. methyl
PT 2-(carboxymethylsulphonyl)-5,7-dichloro-3,8-dihydroxy-6-
PT methyl-9-oxo-9H-xanthene-1-carboxylate.
XX Disclosure; Fig 6 and 7; 117pp; English.
XX The present sequence was used in the development of a novel method
CC for screening for compounds that inhibit or enhance binding of CD28
CC to B7-1.
XX Sequence 475 AA;

Query Match 99.6%; Score 1144; DB 18; Length 475;
Best Local Similarity 99.5%; Pred. No. 1.2e-102;
Matches 215; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGSGVHTVKEVKEVATLSCGHNVSVLELAQTRIYWQKEKKVLTMMSGDMNIWPE 60
|||||

Db 27 glshfcsgvhtvkevekatlscghnsvveelaqtriylwqkekkmvltmmsgdmniwpe 86
|||||

QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTS 120
|||||

Db 87 ykntifdntnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfppts 146
|||||

QY 121 ISDPEITSNIRRICSTSGGFPPLHSLWLENGELNAINITVSDPETELYAVSSKLDF 180
|||||

Db 147 isdpeitnirriictsggfpplhslwleengeelnaintvsgdpetelyavssklidf 206
|||||

QY 181 NMTHSHFMCILIKYGHRLRVNQTFNWNNTKQEHFPDN 216
|||||

Db 207 nmthshfmciklyghlrnvqtnfwnntkqghfpdh 242
|||||

RESULT 14

AAW86004
ID AAW86004 standard; Protein; 488 AA.

XX

AC AAW86004;

XX 15-MAR-1999 (first entry)

XX Human B7-1.5T4.1 protein fusion, specific for human 5T4.

XX Tumour interacting protein; cancer; gene therapy; vector;
KW 5T4 antigen; monoclonal antibody; single chain antibody;
KW mouse; human; B7-1; co-stimulatory molecule.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

OS Chimeric - synthetic.

XX WO9855607-A2.

XX 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB01627.

XX 04-JUL-1997; 97GB-0014230.

XX 04-JUN-1997; 97GB-0011579.

XX 20-JUN-1997; 97GB-0013150.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Bebbington CR, Carroll MW, Ellard FM, Kingsman SM;
PI Myers KA;

XX WPI; 1999-059910/05.

XX N-PSDB; AAV80292.

XX New vector encoding a tumour interacting protein for treating cancer
PT - contains a desired nucleotide sequence and/or protein which
PT recognises tumours, and is used as a gene delivery system to treat
PT cancer

XX Example 5; Fig 2; 82pp; English.

XX This is the amino acid sequence of B7-1.5T4.1, a fusion protein
CC comprising the extracellular domain (amino acids 1-215) of human
CC co-stimulatory molecule B7-1 joined via a flexible peptide linker
CC to an scFv (see AAW86002) derived from murine 5T4 monoclonal
CC antibody. B7-1.5T4.1 cDNA (see AAV80292) can be inserted into vector
CC pCI to allow expression of the fusion protein in mammalian cells.
CC The trophoblast cell surface antigen defined by 5T4 is expressed at
CC high levels on the cells of a wide variety of human tumours. The
CC invention relates to a vector comprising a nucleotide sequence
CC coding for a tumour interacting protein (TIP) and optionally a
CC nucleotide sequence of interest (NOI) which encodes a protein of
CC interest (POI), the vector being capable of delivering the NOI
CC and/or POI to the tumour recognised by the TIP. Delivery can be in
CC vivo or ex vivo. The vector is used to treat cancer, and may also
CC used as a gene delivery system for introducing at least 1 gene
CC encoding a TIP (preferably a tumour binding protein) into a
CC haematopoietic cell lineage. B7-1 is expected to bind specifically
CC to CD28 and CTLA-4 present on human T-cells.

XX Sequence 488 AA;

Query Match 99.5%; Score 1143; DB 20; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.6e-102;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGSGVHTVKEVKEVATLSCGHNVSVLELAQTRIYWQKEKKVLTMMSGDMNIWPE 60
|||||

Db 27 glshfcsgvhtvkevekatlscghnsvveelaqtriylwqkekkmvltmmsgdmniwpe 86
|||||

QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTS 120
|||||

Db 87 ykntifdntnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfppts 146
|||||

QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
 Db 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
 QY 181 NMTNHSFMCCLKYGHRLVNQTFNNTTKQEHFPD 215
 Db 207 NMTNHSFMCCLKYGHRLVNQTFNNTTKQEHFPD 241

RESULT 15
 AAB83836
 ID AAB83836 standard; Protein; 488 AA.
 XX
 AC AAB83836;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Amino acid sequence of a B7-1.5T4.1 fusion protein.
 XX
 KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
 KW hypersensitivity; autoimmune disease; central nervous system disorder;
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
 KW Helicobacter-related disease; immune disorder.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN W0200136486-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 13-NOV-2000; 2000WO-GB04317.
 XX
 PR 18-NOV-1999; 99WO-GB03859.
 PR 15-FEB-2000; 2000GB-0003527.
 PR 02-MAR-2000; 2000GB-0005071.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
 PI Myers KA;
 XX
 DR WPI; 2001-343805/36.
 DR N-PSDB; AAF89730.
 XX
 PT Use of single chain antibody capable of recognizing a disease
 PT associated molecule for manufacturing a medicament for preventing
 PT and/or treating a disease condition associated with disease associated
 PT molecule
 XX
 PS Claim 3; Fig 2; 118pp; English.
 CC
 CC The specification describes the use of a single chain antibody (ScFv),
 CC which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a
 CC disease condition. The ScFv antibody is useful in the manufacture of
 CC a medicament, for affecting a disease in vivo, for preparing a
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for
 CC treating inflammatory diseases including arthritis, hypersensitivity,
 CC autoimmune diseases, cancers, central nervous system disorders
 CC including Parkinson's disease, periodontal diseases, cardiopulmonary
 CC diseases, cardiovascular diseases, gastrointestinal disorders,
 CC infections, diabetes, Helicobacter-related diseases, and other immune
 CC disorders. The present sequence represents a B7-1.5T4.1 fusion protein.
 CC This comprises the N-terminus of the 5T4 ScFv is fused after amino acid
 CC 215 of human B7-1.
 XX
 SQ Sequence 488 AA;

Query Match 99.5%; Score 1143; DB 22; Length 488;
 Best Local Similarity 100.0%; Pred. No. 1.6e-102;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQOTRIYWOKEKKMVLTMMSGDMNIWPE 60
 Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQOTRIYWOKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
 Db 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
 QY 181 NMTNHSFMCCLKYGHRLVNQTFNNTTKQEHFPD 215
 Db 207 NMTNHSFMCCLKYGHRLVNQTFNNTTKQEHFPD 241

Search completed: April 24, 2002, 15:30:21
 Job time: 252 sec

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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:26:09 ; Search time 12.53 seconds
(without alignments)
387.926 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCGVIHVTKEYVA.....LRVNOTFNNTKQEHFPD 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/BCUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	2	US-08-147-772-2
2	1149	100.0	288	2	US-08-456-104-6
3	1149	100.0	288	2	US-08-101-624-23
4	1149	100.0	288	2	US-08-751-767A-6
5	1149	100.0	288	3	US-08-153-262-2
6	1149	100.0	288	3	US-08-479-744A-29
7	1149	100.0	288	4	US-08-280-757B-29
8	1149	100.0	288	4	US-09-159-135-2
9	1149	100.0	288	4	US-08-205-697A-19
10	1149	100.0	288	4	US-08-702-525-19
11	1149	100.0	288	5	PCT-US95-02576-19
12	1149	100.0	473	4	US-09-171-945-131
13	1050	91.4	208	3	US-08-630-172-15
14	1050	91.4	208	4	US-09-375-419-15
15	561	48.8	306	4	US-08-205-697A-17
16	561	48.8	306	4	US-08-702-525-17
17	561	48.8	306	5	PCT-US95-02576-17
18	561	48.8	320	4	US-08-205-697A-2
19	561	48.8	320	4	US-08-702-525-2
20	561	48.8	320	5	PCT-US95-02576-2
21	558	48.6	306	2	US-08-147-772-4
22	558	48.6	306	2	US-08-456-104-8
23	558	48.6	306	2	US-08-101-624-25
24	558	48.6	306	3	US-08-153-262-4
25	558	48.6	306	3	US-08-479-744A-31
26	558	48.6	306	4	US-08-280-757B-31
27	558	48.6	306	4	US-09-159-135-4

28 311 27.1 200 4 US-08-205-697A-9 Sequence 9, Appli
29 311 27.1 200 4 US-08-702-525-9 Sequence 9, Appli
30 311 27.1 200 5 PCT-US95-02576-9 Sequence 9, Appli
31 311 27.1 214 4 US-08-205-697A-11 Sequence 11, Appli
32 311 27.1 214 4 US-08-702-525-11 Sequence 11, Appli
33 311 27.1 214 5 PCT-US95-02576-11 Sequence 11, Appli
34 250.5 21.8 212 4 US-08-702-525-63 Sequence 63, Appli
35 250.5 21.8 212 5 PCT-US95-02576-63 Sequence 63, Appli
36 250.5 21.8 226 4 US-08-702-525-65 Sequence 65, Appli
37 250.5 21.8 226 5 PCT-US95-02576-65 Sequence 65, Appli
38 182 15.8 323 5 PCT-US94-09642-2 Sequence 2, Appli
39 182 15.8 329 2 US-08-456-104-2 Sequence 2, Appli
40 182 15.8 329 2 US-08-101-624-2 Sequence 2, Appli
41 182 15.8 329 3 US-08-479-744A-2 Sequence 2, Appli
42 182 15.8 329 4 US-08-280-757B-2 Sequence 2, Appli
43 182 15.8 329 4 US-08-205-697A-23 Sequence 23, Appli
44 182 15.8 329 4 US-08-702-525-23 Sequence 23, Appli
45 182 15.8 329 5 PCT-US95-02576-23 Sequence 23, Appli

ALIGNMENTS

RESULT 1
US-08-147-772-2
; Sequence 2, Application US/08147772
; Patent No. 5858776
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147.772
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.7e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 27 GLSHFCGVHVTKEVKEVATLSCGHNVSVVEELAQTRIYQKEKKMVLTMMSGDMNIWPE 86
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DB 87 YKNRTIFDTNNLSIVILALRPDSDEGTGECVWLKYEKDAFKREHLAEVTLVKADFPPTPS 146
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DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206
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QY 181 NMTNHSFMCILIKYGLRVNQTFNWNNTTKQEHFPDN 216
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DB 207 NMTNHSFMCILIKYGLRVNQTFNWNNTTKQEHFPDN 242
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RESULT 2
US-08-456-104-6
; Sequence 6, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

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;
;
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-104-6

Query Match      100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.7e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVKADFPPTPS 120
DB 87 YKNRTIFDITNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVKADFPPTPS 146
QY 121 ISDFEPTNIRRIICSTSGGPPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 180
DB 147 ISDFEPTNIRRIICSTSGGPPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 206
QY 181 NMTNHSFMCILIKYGLHVRNVTNNTKOEHPDN 216
DB 207 NMTNHSFMCILIKYGLHVRNVTNNTKOEHPDN 242

RESULT 3
US-08-101-624-23
Sequence 23, Application US/08101624
Patent No. 5942607
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

;
;
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of
; IDENTIFICATION METHOD: soluble protein
; OTHER INFORMATION: hydrophobic
; FEATURE:
; NAME/KEY: extracellular domain
; LOCATION: 1 to 208
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 209 to 235
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: intracellular domain
; LOCATION: 236 to 254
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 19 to 21
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 55 to 57
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 64 to 66
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 152 to 154
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 173 to 175
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 192 to 194
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 1 to 104
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; PUBLICATION INFORMATION:
; AUTHORS: FREEMAN, GORDON J.
```

;; AUTHORS: FREEDMAN, ARNOLD S.
;; AUTHORS: SEGIL, JEFFREY M.
;; AUTHORS: LEE, GRACE
;; AUTHORS: WHITMAN, JAMES F.
;; AUTHORS: NADLER, LEE M.
;; TITLE: B7, A New Member Of The Ig Superfamily With
;; TITLE: Unique Expression On Activated And Neoplastic B Cells
;; JOURNAL: The Journal of Immunology
;; VOLUME: 143
;; ISSUE: 8
;; PAGES: 2714-2722
;; DATE: 15-OCT-1989
;; RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262
US-08-101-624-23

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.7e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 86

QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146

QY 121 ISDEIPTSNIRRIICSTSGGPPHLSWLENGEELNAINTTVSQDPETELAVSSKLD 180
DB 147 ISDEIPTSNIRRIICSTSGGPPHLSWLENGEELNAINTTVSQDPETELAVSSKLD 206

QY 181 NMTNHSPMCLIKYGLRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTNHSPMCLIKYGLRVNQTFFNNTTKQEHFPDN 242

.. RESULT 4
US-08-751-767A-6
; Sequence 6, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,767A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164091
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-751-767A-6

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.7e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 86

QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146

QY 121 ISDEIPTSNIRRIICSTSGGPPHLSWLENGEELNAINTTVSQDPETELAVSSKLD 180
DB 147 ISDEIPTSNIRRIICSTSGGPPHLSWLENGEELNAINTTVSQDPETELAVSSKLD 206

QY 181 NMTNHSPMCLIKYGLRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTNHSPMCLIKYGLRVNQTFFNNTTKQEHFPDN 242

.. RESULT 5
US-08-153-262-2
; Sequence 2, Application US/08153262
; Patent No. 6071716
; GENERAL INFORMATION:
; APPLICANT: FREEMAN, GORDON J.
; APPLICANT: FREEDMAN, ARNOLD S.
; APPLICANT: NADLER, LEE M.
; TITLE OF INVENTION: DNA Encoding B7, A New Member
; TITLE OF INVENTION: Of The IgG Superfamily With Unique Expression On
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Dana-Farber Cancer Institute
; STREET: 44 Binney Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02115
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
; COMPUTER: IBM Personal System 2; Model 30
; OPERATING SYSTEM: MS/DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/751,306
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HART, JULIA D.
; REGISTRATION NUMBER: 33132
; REFERENCE/DOCKET NUMBER: DFCI-116.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255-8900
; TELEFAX: (203) 259-2846
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

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RESULT      6
US-08-479-744A-29
; Sequence 29, Application US/08479744A
; Patent NO. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: Nos. 6084067el CtlA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993

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; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; FEATURE: for CD28 T cell surface antigen; transmembrane protein
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of
; IDENTIFICATION METHOD: soluble protein
; OTHER INFORMATION: hydrophobic
; FEATURE:
; NAME/KEY: extracellular domain
; LOCATION: 1 to 208
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 209 to 235
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: intracellular domain
; LOCATION: 236 to 254
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 19 to 21
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 55 to 57
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; NAME/KEY: N-linked glycosylation
; LOCATION: 64 to 66
; IDENTIFICATION METHOD: similarity with known
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; LOCATION: 173 to 175
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; NAME/KEY: N-linked glycosylation
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; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 192 to 194
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; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation

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; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 1 to 104
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; PUBLICATION INFORMATION:
; AUTHORS: FREEDMAN, GORDON J.
; AUTHORS: SEGIL, JEFFREY M.
; AUTHORS: LEE, GRACE
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
; TITLE: B7, A New Member Of The Ig Superfamily With
; TITLE: Unique Expression On Activated And Neoplastic B Cells
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
; US-08-479-744A-29

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Query Match 100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. NO. 4.7e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYWKQKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYWKQKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPDSDEGYECVVLKYKDAFKREHLAEVTLVKADFPPTPS 120
Db 87 YKNTIFDITNNLSIVILALRPDSDEGYECVVLKYKDAFKREHLAEVTLVKADFPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
QY 181 NMTNHSFMCILIKYGLRVNQTFNNWTTKQEHFPDN 216
Db 207 NMTNHSFMCILIKYGLRVNQTFNNWTTKQEHFPDN 242

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RESULT 7
US-08-280-757B-29
; Sequence 29, Application US/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
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; NAME/KEY: N-linked glycosylation
; LOCATION: 177 to 179
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
;
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 192 to 194
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
;
; NAME/KEY: N-linked glycosylation
; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
;
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 1 to 104
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
;
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
;
; PUBLICATION INFORMATION:
; AUTHORS: FREEMAN, GORDON J.
; AUTHORS: FREEDMAN, ARNOLD S.
; AUTHORS: SEGIL, JEFFREY M.
; AUTHORS: LEE, GRACE
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
;
; TITLE: B7, A New Member Of The Ig Superfamily With
; TITLE: Unique Expression On Activated And Neoplastic B Cells
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
;
; RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
;
; US-08-280-757B-29
;
;
; Query Match 100.0%; Score 1149; DB 4; Length 288;
; Best Local Similarity 100.0%; Pred. No. 4.7e-113;
; Matches 216; Conservative 0; Mismatches 0; Indels 0;
;
; Qy 1 GLSHFCSGVHVTKEVKEVATLSCGHNVSVBELAQTRIYWQEKKKMVLTMMSGDMNLTW
; Db 27 GLSHFCSGVHVTKEVKEVATLSCGHNVSVBELAQTRIYWQEKKKMVLTMMSGDMNLTW
;
; Qy 61 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLTSVKADFP
; Db 87 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLTSVKADFP
;
; Qy 121 ISDEIPTSNTRRICSTSGGFPPEHLSWLENGELNAINTVSQDPETELAYVSSKIK
; Db 147 ISDEIPTSNTRRICSTSGGFPPEHLSWLENGELNAINTVSQDPETELAYVSSKIK
;
; Qy 181 NMTTNHSPMCLIKYGHLRVNOTFNWNTTKQEHFPDN 216
; Db 207 NMTTNHSPMCLIKYGHLRVNOTFNWNTTKQEHFPDN 242
;
; RESULT 8
; US-09-159-135-2
; Sequence 2, Application US/09159135
; Patent No. 6149905
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian

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; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/159,135
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/147,772
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of
; IDENTIFICATION METHOD: soluble protein
; OTHER INFORMATION: hydrophobic
; FEATURE:
; NAME/KEY: extracellular domain
; LOCATION: 1 to 208
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 209 to 235
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: intracellular domain
; LOCATION: 236 to 254
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 19 to 21
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 55 to 57
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 64 to 66

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; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 152 to 154
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 173 to 175
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 177 to 179
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 192 to 194
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 1 to 104
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; PUBLICATION INFORMATION:
; AUTHORS: FREEMAN, GORDON J.
; AUTHORS: FREEDMAN, ARNOLD S.
; AUTHORS: SEGIL, JEFFREY M.
; AUTHORS: LEE, GRACE
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
; TITLE: B7, A New Member Of The Ig Superfamily With
; TITLE: Unique Expression On Activated And Neoplastic B Cells
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
; US-09-159-135-2

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Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.7e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GLSHFCSGVHTVTKVEKAVATLSCGHNVSVVEELAQTRIYWKQKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVHTVTKVEKAVATLSCGHNVSVVEELAQTRIYWKQKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDIITNNLSIVILALRPDSDEGYECVWLKYKDAFKREHLAEVTLVSKADFPPTS 120
Db 87 YKNTIFDIITNNLSIVILALRPDSDEGYECVWLKYKDAFKREHLAEVTLVSKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINITVSQDPETELYAVSSKLDF 180
Db 147 ISDFEPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINITVSQDPETELYAVSSKLDF 206
QY 181 NMTTNHSFMCILIKYGHURVNOTFNNTTKQEHFPDN 216

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Db 207 NMTHSFMCILIKYGLHVRNQTNNWNTTKQEHFPDN 242

RESULT 9

US-08-205-697A-19
; Sequence 19, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-205-697A-19

Query Match 100.0%; Score 1149; DB 4; Length 288;

Best Local Similarity 100.0%; Pred. No. 4.7e-113;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVHVTKEVAVATLSGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVHVTKEVAVATLSGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 86
Qy 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTS 146
Qy 121 ISDFEIPTSNRRICSTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 180
Db 147 ISDFEIPTSNRRICSTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206
Qy 181 NMTHSFMCILIKYGLHVRNQTNNWNTTKQEHFPDN 216
Db 207 NMTHSFMCILIKYGLHVRNQTNNWNTTKQEHFPDN 242

RESULT 10

US-08-702-525-19
; Sequence 19, Application US/08702525
; Patent No. 6294660
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.

; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Lee
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-525-19

Query Match 100.0%; Score 1149; DB 4; Length 288;

Best Local Similarity 100.0%; Pred. No. 4.7e-113;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVHVTKEVAVATLSGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVHVTKEVAVATLSGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 86
Qy 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTS 146
Qy 121 ISDFEIPTSNRRICSTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 180
Db 147 ISDFEIPTSNRRICSTSGGFPPEHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206
Qy 181 NMTHSFMCILIKYGLHVRNQTNNWNTTKQEHFPDN 216
Db 207 NMTHSFMCILIKYGLHVRNQTNNWNTTKQEHFPDN 242

RESULT 11

PCT-US95-02576-19
; Sequence 19, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston

Gaps 0;

QY 9 VHVTKVEKAVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNINPEYKNRTIFD 68
Db 1 VHVTKVEKAVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNINPEYKNRTIFD 60
QY 69 ITNNLSIVILALRPSDEGTGTCVVLKYEKDAFKREHLAEVTLVSQDPETELAVSSKLDPMNTTNSF 128
Db 61 ITNNLSIVILALRPSDEGTGTCVVLKYEKDAFKREHLAEVTLVSQDPETELAVSSKLDPMNTTNSF 120
QY 129 SNIRRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELAVSSKLDPMNTTNSF 188
Db 121 SNIRRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELAVSSKLDPMNTTNSF 180
QY 189 MCLIKYGLHVRNQTNNWNTTKOEHPDN 216
Db 181 MCLIKYGLHVRNQTNNWNTTKOEHPDN 208

RESULT 14

US-09-375-419-15
; Sequence 15, Application US/09375419
; Patent No. 6264950
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; TITLE OF INVENTION: LYMPHOCYTE VETO
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/375,419
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-375-419-15

Query Match 91.4%; Score 1050; DB 4; Length 208;
Best Local Similarity 95.7%; Pred. No. 7.6e-103;
Matches 199; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 9 VHVTKVEKAVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNINPEYKNRTIFD 68
Db 1 VHVTKVEKAVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNINPEYKNRTIFD 60
QY 69 ITNNLSIVILALRPSDEGTGTCVVLKYEKDAFKREHLAEVTLVSQDPETELAVSSKLDPMNTTNSF 128
Db 61 ITNNLSIVILALRPSDEGTGTCVVLKYEKDAFKREHLAEVTLVSQDPETELAVSSKLDPMNTTNSF 120

QY 129 SNIRRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELAVSSKLDPMNTTNSF 188
Db 121 SNIRRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELAVSSKLDPMNTTNSF 180
QY 189 MCLIKYGLHVRNQTNNWNTTKOEHPDN 216
Db 181 MCLIKYGLHVRNQTNNWNTTKOEHPDN 208

RESULT 15

US-08-205-697A-17
; Sequence 17, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-205-697A-17

Query Match 48.8%; Score 561; DB 4; Length 306;
Best Local Similarity 50.7%; Pred. No. 4.3e-51;
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTKVEKAVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNINPEYKNRTIFD 71
Db 42 LSKSVKDKVLLPCRYNSPHEDESDRIYQKHDKVLSVIAKGLKVPYKNRTLYDNT- 100
QY 72 NLSVILALRPSDEGTGTCVVLKYEKDAFKREHLAEVTLVSQDPETELAVSSKLDPMNTTNSF 131
Db 101 TYSIIILGLVSDRGTYSCVQKRGTYEVKHLALVKLSIKADFTNITESGNPSADT 160
QY 132 RRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELAVSSKLDPMNTTNSF 191
Db 161 KRITCFASGGPKPFRFSLNGLRELPGINTTISQDPESELITISSQLDFNTRNHTIKCL 220
QY 192 IKYGLHVRNQTNNWNTTKOEHPDN 216
Db 221 IKYGDHVSDEFTWEKPPDP-PDS 244

Search completed: April 24, 2002, 15:30:40
Job time: 271 sec